2017

Population history and dispersal of Taiwanese Indigenous people

BOSTON UNIVERSITY

SCHOOL OF MEDICINE

Thesis

POPULATION HISTORY AND DISPERSAL OF TAIWANESE INDIGENOUS PEOPLE

by

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B.A., National Taiwan University, 2013

Submitted in partial fulfillment of the

requirements for the degree of

Master of Science

2017

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ACKNOWLEDGMENTS

The completion of this research is due to the efforts and support of many individuals. First of all, I would like to thank the members of my research committee for their invaluable assistance during the research. I thank Dr. James Pokines, for the patience and effort he put into my work. I would sincerely like to thank Dr. Michael Pietrusewsky for the comments, feedback, and suggestions that he made for my research. I would also like to thank my third reader, Dr. Jonathan Bethard, for his help in the development of my research. I would also like to thank Dr. Farzad Mortazavi for his assistance in statistics. I would like to pay my regards to the program for providing me the resources for the research. I would also like to thank Ms. Samantha Calderazzo, who helped me refine my English.

I would like to show my special thanks to Dr. S. T. Hsieh, Chairman of the Graduate Institute of Anatomy and Cell Biology, National Taiwan University and Dr. H. K. Tsai, Professor Emeritus of the Graduate Institute of Anatomy and Cell Biology, National Taiwan University, for granting me access to the collection. I thank Dr. Tsai for his generous help and the priceless information that he provided. It is a great honor to work with a legendary scholar. His assiduous and studious ethic has become a role model for me. I would also like to thank Dr. K. S. Lu, Mr. K. M. Chang, and Ms. P. Y. Tsai from the Graduate Institute of Anatomy and Cell Biology, National Taiwan University, for their assistance in my research.

In the Department of Anthropology, National Taiwan University, I would like to thank to Dr. M. L. Chen, Dr. Y. P. Chen, and Dr. P. C. Chen for their help in developing

this research. I thank Dr. M. L. Chen for introducing me to Dr. H. K. Tsai. Dr. Chen is the origin of this research, if it were not her, this research would never be developed. I also thank Dr. Y. P. Chen for his unselfish help. At the time I was struggling with the materials, he generously opened all his resources for me to access. A special thank to my late professor Dr. P. C. Chen, a professor that was always there for help no matter how late. He was the professor that every student wishes that he had. I would also like to thank Dr. K. T. Li from Academia Sinica, Taiwan, for his support since my time as an undergraduate. Dr. Li is an influential mentor in my life. If it were not him, I would never have been an anthropologist.

My sincere thanks also goes to my employers and colleagues over these years. I appreciate their encouragement and support. It was their considerateness that made it possible to pursue my education.

Finally, I would like to show my gratitude to all individuals that had helped me during these days. Special thanks to my cohort, for helping me immerse into life in the U.S. I also need to thank my friends and family for the support in this research and in my life. I would like to thank them for being understanding at the times when I was not around for birthdays, holidays, or special events.

POPULATION HISTORY AND DISPERSAL OF TAIWANESE INDIGENOUS PEOPLE

PATRICIA BIAN

ABSTRACT

The purpose of this study is to present the biological affinity of four Taiwanese Indigenous groups. Previous studies based on linguistics and ethnography had shown that there are differences between the indigenous groups in Taiwan (Ferrell 1969; Utsurikawa *et al.* 1935). Archaeological remains also indicate that there was a wide variety of groups (Tsang 1995). In order to provide some biological evidence for this issue, the present research estimated the biodistance from both cranial measurements and non-metric cranial traits between the four Taiwanese Indigenous groups (Atayal, Bunun, Babuza, and Pazeh) from modern collections.

It is hypothesized that the Taiwanese Indigenous groups would have significant biological differences: the Atayal and Bunun samples (mountain indigenous) would cluster, while the Babuza and Pazeh (lowland indigenous) would cluster separately. The two hypotheses were supported from both craniometric and non-metric data in the present study.

Limited comparison with groups from other areas was also performed in order to examine the possible dispersal pattern of the Taiwanese Indigenous groups. Craniometric data from three samples (South Japan, Philippines, and Hainan) from the William W. Howells Craniometric Data Set and non-metric data of four samples (Philippines, South China, Southeast Asians, and Okinawa) from Fukumine *et al.* (2006) were used. Since

the popular hypothesis of the Austronesians' origin suggests that there was intensive movement between Taiwan and Philippines (e.g., Bellwood 1988; Diamond 2000; Melton *et al.* 1995; Solheim 1988; Su *et al.* 2000; Trejaut *et al.* 2005), it is hypothesized that the Taiwanese Indigenous groups would show the closest affinity with the samples from Philippines while the other groups would be in another cluster. However, this hypothesis is not supported in the present study. The result showed that the Taiwanese Indigenous groups and those from the Philippines are relatively distant. This supports the hypothesis of Tsang (2012) that the early dispersal of Austronesian groups may have occurred several times through multiple routes to Taiwan and the Philippines.

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LIST OF ABBREVIATIONS

ASB	Biasterionic Breadth
AUB	Biauricular Breadth
BBH	Basion-Bregma Height
BNL	Cranial Base Height
BPL	Basion-Prosthion Length
DKB	Interorbital Breadth
DKR	Dacryon Radius
DKS	Dacryon Subtense
EKB	Biorbital Breadth
EKR	Ectoconchion Radius
FMB	Bifrontal Breadth
FMR	Frontomalare Radius
FRC	Frontal Chord
GLS	Glabella Projection
GOL	Maximum Cranial Length
ICC	Intraclass Correlation Coefficients
IML	Malar Length, inferior
JUB	Bijugal Breadth
MDH	Mastoid Height
MMD	Mean Measure of Divergence
NAR	Nasion Radius

NAS	Nasio-frontal Subtense
NDS	Naso-dacryal Subtense
NLB	Nasal Breadth
NLH	Nasal Height
NOL	Nasio-occipital Length
NPH	Nasion-prosthion Height
NTU	National Taiwan University
OBB	Orbital Breadth
OBH	Orbital Height
PAC	Parietal Chord
PRR	Prosthion Radius
SSR	Subspinale Radius
STB	Bistephanic Breadth
UPGMA	Unweighted Pair Group Method with Arithmetic Mean
WMH	Cheek Height
WNB	Simotic Chord (Least Nasal Breadth)
XCB	Maximum Cranial Breadth
XFB	Maximum Frontal Breadth
XML	Malar Length, maximum
ZMB	Bimaxillary Breadth
ZMR	Zygomaxillare Radius
ZOR	Zugoorbitable Radius

ZYB	Bizygomatic Breadth

CHAPTER 1: INTRODUCTION

The identity of Taiwanese Indigenous[1] (i.e., Indigenous Taiwanese; Executive Yuan 2015) is a subject of extensive debate in the field of anthropology. During the Japanese Colonial Period (1895-1945), scholars divided the indigenous people in Taiwan into nine different groups based on ethnographical research: Atayal, Saisiat, Bunun, Tsou, Amis (Pangtsah), Rukai, Paiwan, Puyuma (Panapanayan) and Yami (Tau) (Utsurikawa *et al.* 1935). Eight of the nine groups (Atayal, Saisiat, Bunun, Tsou, Amis, Rukai, Paiwan and Puyuma) inhabited the more mountainous region of Taiwan, which led to less acculturation with the Han Chinese. The Yami inhabited Lanyu, an island located in southeast Taiwan (Figure 1.1). The lowland indigenous groups, who were primarily located in the western coast of the island, had more interactions with populations outside the island. According to Nakamura (1936), based on the *House Registration of the Taiwan's Aboriginal Document* during the Dutch Rule period (early 17th century), there were at least eight lowland indigenous groups in Taiwan (Siraya, Hoanya, Babuza, Pazeh, Papora, Taokas, Ketagalan, and Kavalan). Further studies based on linguistic and cultural evidence suggest that there are more groups in Taiwan (Lee 1992; Tsuchida 1985).

According to linguistic studies, all the modern indigenous groups in Taiwan speak an Austronesian language (Lewis 2009). In fact, one of the most popular assumptions is that people inhabiting Taiwan after the early Neolithic period (the Tapenkeng Culture, 7000-4700 BP) and before the entry of Chinese and European periods (around 17th

[1] The non-Han Chinese people in Taiwan were called aboriginal Taiwanese or Taiwanese aborigines previously. The official label was changed to Taiwanese Indigenous or Indigenous Taiwanese on January 4, 2002 (Council of Indigenous Peoples 2010).

century) spoke Austronesian languages (Lee 2011; Tsang 1995, 2012). During this period, the only people in Taiwan were Austronesian speakers, and it is believed that they were the early ancestors of the modern Taiwanese Indigenous. Therefore, the discussions of the Taiwanese Indigenous are often in the context of this linguistic affiliation.

Figure 1.1. General distribution of the nine indigenous groups in Taiwan (redrawn from Utsurikawa *et al.* 1935:iv).

Austronesians are people who speak the languages of the Austronesian language family. The distribution of the Austronesian-speaking people includes an area from Madagascar in the west to Easter Island in the east (Figure 1.2). The majority groups

from Taiwan, Philippines, Malaysia, Indonesia, East Timor, Brunei, Madagascar, Micronesia, Polynesia, and the non-Papuan people of Melanesia are considered Austronesian-speaking people (Lewis 2009).

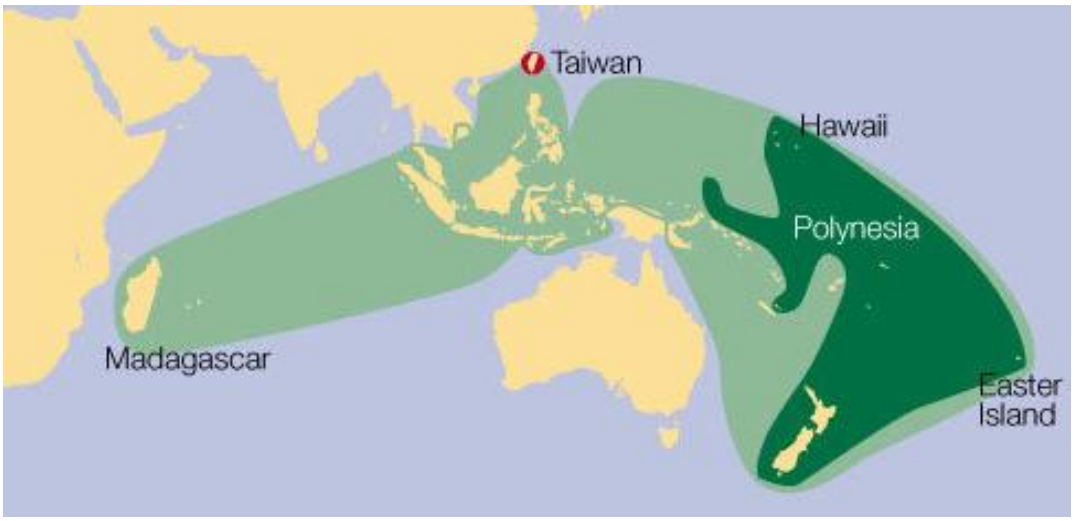

Figure 1.2. General distribution of the Austronesians (modified from Diamond 2000:709).

Although linguistic and cultural studies have shown that there are differences between Taiwanese Indigenous groups, few studies in biological anthropology have examined this assumption. It is important to note that Austronesian groups were actually defined by language; therefore, it is necessary to examine whether they were also biologically different.

Several anthropometric studies and genetic research suggest that there are biological differences between the populations (Chai 1967; Chen *et al*. 2007; Lin and Broadberry 1998; Lin *et al.* 2000; Melton *et al.* 1995; Su *et al.* 2000; Trejaut *et al.* 2005; Tsai and Lu 2003). These studies suggest that different indigenous groups can be well

separated by different biological features. However, the anthropometric studies only provide rough conclusions using anthroposcopic observation or measurements.

Though genetic methods may provide more exact results, there are some problems, including small sample sizes, with the research done so far. For example, Su *et al.* (2000) examined a sample size of only 6 individuals. However, the most crucial challenge of applying either anthropometric or modern genetic methods to Taiwanese Indigenous is that the identity of modern Taiwanese Indigenous can be problematic. There are two main reasons. First, the modern Taiwanese Indigenous groups are mixed, especially in the past 80 years. The development of the country led to increasing admixture among the people from different tribes, and new education dominated by Han Chinese people reduced the influence of traditional marriage taboos or preferences. Second, the assumed ethnic affiliation of some individuals or tribes may not be correct. For example, a person assumed to be Amis today might actually be of Atayal or Rukai ancestry. This is due to certain political issues during the Japanese Colonial Period; some individuals were forced to move to other places for increased government control (Ino 1904, n.d.; Wang 2000; Yanayihara 1929). There are also situations when after times of rebellion, individuals may have claimed themselves to be from a different ethnic group in order to avoid punishment. Based on these reasons, after nearly a century, many modern Taiwanese Indigenous people may not know their "real" ethnic identity. Therefore, a perspective from skeletal biology may provide a better understanding of the relationships among Taiwanese Indigenous populations.

The study of biological distance is a way to measure the divergence of populations based on polygenic traits (Buikstra *et al.* 1990). Variations in bone morphology may reflect genetic relatedness between populations. Individuals or populations that are more similar in bone morphology are considered to have a relatively closer affinity. In other words, biodistance studies can be useful in reconstructing population history and structure (Buikstra *et al.* 1990).

Therefore, one purpose of the present study is to measure the degree of biological affinity between the Taiwanese Indigenous groups. As mentioned above, several studies have attempted to answer this question using modern genetic data (Chen *et al.* 2007; Jin *et al.* 1999*;* Lin and Broadberry 1998; Lin *et al.* 2000; Melton *et al.* 1995; Su *et al.* 2000; Trejaut *et al.* 2005; Yuasa *et al.* 2001). Though the relationship of different populations may differ from study to study, all of this research suggests that there are certain levels of biological differences among Taiwanese Indigenous. In other words, the division of Taiwanese Indigenous populations may be attributed to biology as well as ethnography.

Recent studies of Austronesian-speaking peoples also suggest that the Taiwanese Indigenous may be the possible origin of the Austronesian-speaking peoples (Bellwood 1988; Diamond 2000; Melton *et al.* 1995; Trejaut *et al.* 2005). This hypothesis was first proposed by Shutler and Marck (1975) based on archaeological and linguistic evidence. Although the research done by Shutler and Marck (1975) is now considered to be out of date, other linguistic research has come up with similar assumptions due to the diversity of Austronesian languages in Taiwan (Lee 2011). In linguistic studies, based on Sapir's (1916) theory, the area with the greatest linguistic diversity is the area most likely to be

the homeland of a linguistic group. This assumption is also supported by other researchers (Dyen 1956; Kroeber 1955). Though this theory has some flaws, it is noted that in Taiwan, the area with the greatest linguistic diversity is located in the central area, more specifically in the basin area of Nantou County (Figure 1.3) (Lee 2011). Therefore, four indigenous populations (Atayal, Bunun, Babuza and Pazeh) in the central area of Taiwan were used in this study. Since these four populations were separated from each other both linguistically and culturally, it is hypothesized that the four populations can also be separate based on biological differences.

Figure 1.3. Taiwan map. Nantou is in dark gray (redrawn from Executive Yuan 2015:49).

However, other research suggests that the origin of the Austronesians is actually in Southeast Asia, with Taiwan acting as a transfer stop in the middle (Solheim 1988; Su *et al.* 2000). With this assumption, it is thought that the Philippines or mainland Southeast Asia is the most likely origin, and that Taiwan played an important role as a transfer stop in the dispersal to the Polynesians. A new hypothesis summarized in Tsang (2012), based on comparing archaeological evidence with surrounding areas, suggests that the dispersal of proto-Austronesian populations may have occurred multiple times and with multiple routes to Taiwan and the Philippines.

Since Taiwan was placed in a crucial location in the dispersal of the Austronesian-speaking people in both theories, an understanding of the dispersal of the Taiwanese Indigenous is necessary. Regarding the origin of the Taiwanese Indigenous, Chen (2002, 2014) and Tsang (2012) both pointed out that archaeological evidence had shown that there is little relation between Taiwan and regions to the north, such as the Ryukyu Islands and southern Japan. In fact, based on archaeological evidence, the most likely route is either from southeast China or the Philippines. However, results from Pietrusewsky and Chang (2003) show that the ultimate source of Taiwanese Indigenous population may be from eastern and northeastern Asia. Since a perspective from biological anthropology regarding the relationship between Taiwanese Indigenous populations and other populations around Taiwan is necessary, a comparison with surrounding areas is included in the present study. In addition to the issue of the origin of the Taiwanese Indigenous (which often linked with the origin of the Austronesians), the migration of the indigenous populations within the island is also important. Lee (2011)

pointed out that knowing the dispersal pattern of the Taiwan Indigenous populations within the island is a fundamental part of understanding the language diversity. He outlined the potential dispersal pattern within the island based on linguistic and historical documents. However, a biological perspective is necessary. In the present study, an examination of Lee's assumption will be provided. Lee (2011) suggested that the Atayal and Bunun populations inhabited the Nantou area around 4000 B.P., while the Babuza and Pazeh populations together migrated to this area around the 19th century. Therefore, it is hypothesized that the Atayal and Bunun populations will be clustered together, while the Babuza and Pazeh will from another cluster.

Since using modern samples as material for this kind of study can be problematic, it is better to use archaeological collections. However, due to various taphonomic processes, the preservation of the bones may be poor, so measurements may not be able to be taken completely. Therefore, in the present study, both metric and non-metric data were used, and the results were checked to examine correlation.

In the present study, four Taiwanese Indigenous groups (Atayal, Bunun, Babuza and Pazeh) in the middle part of Taiwan are examined. The hypothesis is that the four groups should demonstrate biological differences based on metric and non-metric data. In other words, the indigenous groups in Taiwan are not just a linguistic or cultural group, but actually differ biologically. Furthermore, the Atayal and Bunun, as the mountain indigenous, should show one cluster, while the Babuza and Pazeh, as the lowland indigenous, should show another cluster. Since the popular hypotheses of the Austronesians' origin both suggest that there was intensive population movement

between Taiwan and Philippines (e.g., Bellwood 1988; Diamond 2000; Melton *et al.* 1995; Solheim 1988; Su *et al.* 2000; Trejaut *et al.* 2005), the another hypothesizes that the Taiwanese Indigenous groups will show the closest affinity with the groups from Philippines and that the rest of the groups will be in another cluster. In other words, though the direction may not be known, there was population movement between Taiwan and Philippines.

CHAPTER 2: THE TAIWANESE INDIGENOUS

The history of studies of the Taiwanese Indigenous started in the 20th century during the Japanese Colonial Period (1895-1945). Ino and Awano (1900) first published a report about the indigenous populations in Taiwan. Based on linguistic and ethnographic research, they divided the Taiwanese Indigenous into eight groups: Atayal, Vonum (Bunun), Amis, Tsou, Tsarisen, Puyuma, Spayowan, and Peipo (the lowland indigenous) (Figure 2.1). After that, different divisions have been proposed by other researchers (Figure 1.1) (Fujisaki 1930; Kojima 1913-1921; Mori 1912; Sayama 1913-1921; Torii 1910; Utsurikawa *et al.* 1935). In some studies, history, material culture, customs and area of habitation (lowland or mountain) were also take into consideration. Though much research proposed multiple ways of dividing the populations of Taiwanese Indigenous, only slight differences were found between each result. For a long period, the nine divisions were widely accepted and used. It is noted that during that time, the focus was primarily on the mountain indigenous.

Meanwhile, studies from a biological perspective were also conducted during the Japanese Colonial Period. Japanese scholars such as Torii focused on methods including anthropometry, blood type and palm prints (Torii 1910; Tsai and Lu 2003). Research involving skulls, vertebrae or teeth was also done from 1922 to 1935 (Tsai and Lu 2003, pers. comm.). Systematic studies started in 1936, led by Kanaseki of the Imperial University of Taipei (now National Taiwan University). The research included somatometry, osteometry, blood type, dermatoglyphics and the growth rate of children

(Kanaseki 1978; Tsai and Lu 2003; Tsai, pers. comm.). The results of these studies showed that there were biological differences between the different indigenous groups.

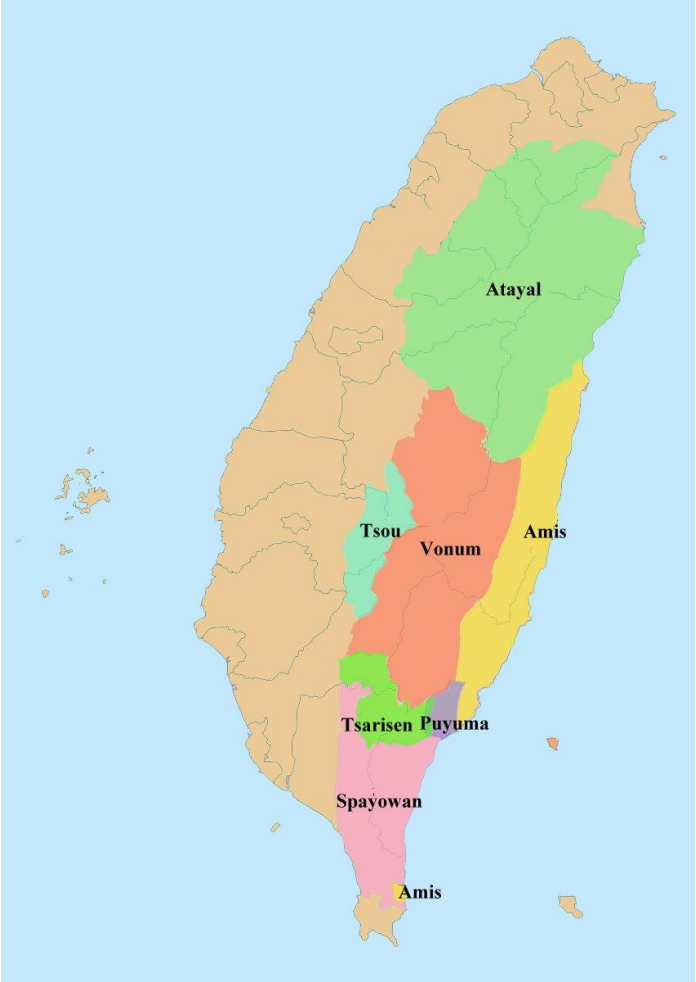

Figure 2.1. Division of the indigenous groups in Taiwan (redrawn from Ino and Awano 1900:iii).

After the Japanese Colonial Period (1895-1945), the research perspective on Taiwanese Indigenous continued to follow the work of Dr. Kanaseki. As students of Kanaseki, scholars such as H. K. Tsai, T. L. Tsai, and J. C. Yu inherited the work of the Japanese scholars. In addition, modern genetic methods led to new ways to examine the relationship among the Taiwanese Indigenous groups. Recently, researchers have used

materials such as mtDNA, Y-chromosome isoenzyme, polymorphism and immunoglobulin in their studies (Chen *et al*. 2007; Lin 2001; Lin and Broadberry 1998; Lin *et al.* 2000; Melton *et al.* 1995; Su *et al.* 2000; Trejaut *et al.* 2005).

The Dispersal of the Taiwanese Indigenous

The dispersal of the Taiwanese Indigenous can be discussed in two parts; the first part is migration within the island, and the second is the search for the homeland of the Taiwanese Indigenous. As mentioned above, discussions of Taiwanese Indigenous are often in the context of the Austronesians. Therefore, questions of Taiwanese Indigenous groups' origins would often be contextualized within the framework of the dispersal of the Austronesians, so the origin of the Austronesians is a key point in understanding the origins of the Taiwanese Indigenous.

Migration within the Island

There are three major mechanisms of the migration of the Taiwanese Indigenous populations within the island: pressure from other groups and the environment, cultural taboos, and governmental force.

Pressure from other Groups and the Environment

Taiwan is an island about 400 kilometers long and 150 kilometers wide (Figure 2.2). Although the area of the island is less than 36,000 km^2, there are over 260 mountains that are over 3,000 meters in height. In fact, over two-thirds of the island is

covered by mountains and hills (Executive Yuan 2015). Therefore, areas that are suitable for human habitation are very limited.

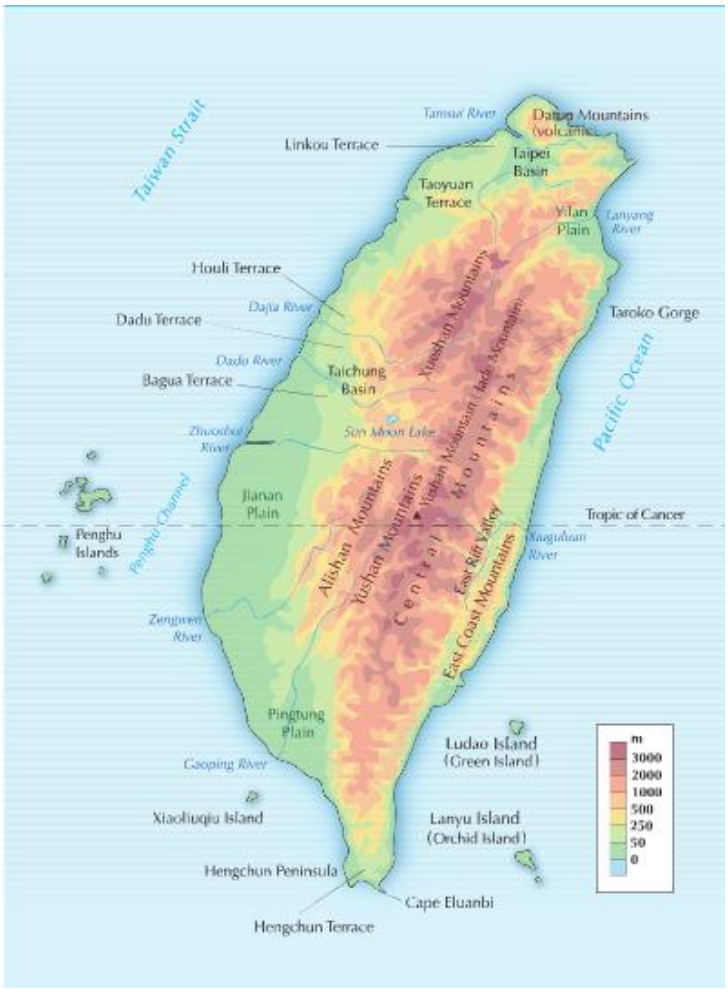

Figure 2.2. Taiwan and nearby islands (Executive Yuan 2015:41).

Since the areas of the lowlands were very limited, the competition between populations for resources may have been very high. Historic, linguistic and archaeological evidence indicate that populations may migrate when facing more powerful groups (Lee 2011; Sayama 1913-1921; Utsurikawa *et al.* 1935). For example, the Qauqaut (one of the lowland indigenous groups) were forced to move due to the

expansion of Atayal (Lee 2011; Mabuchi 1953, 1954). The Qauqaut originally occupied the area around the midstream of the Li Wu River (east coast of the island), later moving toward to the estuary. Finally, when the Atayal occupied the whole valley of the Li Wu River, the Qauqaut moved to the far north, away from the Li Wu River entirely.

Another typical example of the influence of other groups and the environment is the migration of the Bunun people. According to their oral history, the Bunun people originally inhabited the lowland area in the western part of the island. Due to lowland indigenous neighbors who were more powerful, and the entry of the Han Chinese people, they moved to the southern part of Nantou area. However, as the Bunun continued to increase in number, the original hunting area and farmland could not support the entire group. Therefore, the population expanded further inland toward the southeast and south, then to the west and southwest (Haisul Palalavi 2006; Huang 1992; Mabuchi 1953, 1954, Sayama 1913-1921; Utsurikawa *et al.* 1935). Similarly, the lowland indigenous groups were also forced to move to the inland due to the entry of the Han Chinese people. For example, during the early 19th century, there were multiple migrations of the Babuza and Pazeh groups, due to the Han Chinese people, to the Puli basin (Hung 2006).

Cultural Taboos

For many Taiwanese Indigenous groups, cultural taboos are one of the most common reasons why groups might move (Sayama 1913-1921). For example, in Atayal culture, several events caused people to abandon their traditional territory (Sayama 1913-1921). The brown spotted pit viper (*Trimeresurus mucrosquamatus*) was viewed as a

representation of an evil spirit. When the snake appears in the house, Atayal people believe that the house was occupied by the evil spirit and therefore they should move to other areas immediately. Another event causing home abandonment is when someone died accidentally, since it is considered that the family was being cursed. In order to prevent further accidents, people move to another place immediately. Some situations similar to this phenomenon can affect the whole group, causing the migration of the entire group. Such events might include an epidemic or natural disaster. When people are moving due to "evil spirits", it is common in many Taiwanese Indigenous groups to abandon the entire household without bringing any possessions.

Governmental Force

The influence of the government always played an important role in the dispersal of the Taiwanese Indigenous. As mentioned in Chapter 1, during the Japanese Colonial Period, governmental policies forced entire groups to move to certain locations in order for the government to exert easier control (Ino 1904, n.d.; Wang 2000; Yanayihara 1929). One of the outcomes of this policy was that the government might force tribes that were close to each other to move together to a certain area for centralized management. This caused tribes of different groups to mix with each other. In some cases, a dominant group may assimilate the other groups. It is also noted that this may reduce the influence of marriage taboos. Another government policy was to separate a tribe (or group), forcing people from the same tribe (or group) to move to different places in order to isolate them. This is a common method after rebellion or when the government faced

multiple opposition groups. Avoiding punishment from the government may also be a reason to move. After times of rebellion, people may move to the area of another group or claim themselves as being from a different ethnic group in order to keep safe or avoid punishment from the government. It is noted that though the process was not as violent as the Japanese Colonial Period, the government policy still influenced the movement of the Taiwanese Indigenous before or after this time.

The Origin of the Austronesian-Speaking Peoples

The homeland of the Austronesians, as mentioned above, is controversial. Shutler and Marck (1975) first posited, based on archaeological and linguistic data, that Taiwan might be the origin of the Austronesians, whose descendants then moved on to settle in the Philippines, New Guinea, and Indonesia before 4500 B.C. and eventually into Remote Oceania. However, with more archaeological and biological evidence, two major theories (Figures 2.3 and 2.4) were proposed to answer this question.

The first theory, as Shutler and Marck (1975) suggested, is the "out of Taiwan" theory. The general dispersal pattern is presented in Figure 2.3. Though the work done by Shutler and Marck (1975) is now considered to be out of date, this research influenced many later researchers. Subsequent research by linguists supports this hypothesis due to the huge divergence in languages within Taiwanese groups (Bellwood 1991; Blust 1988; Dyne 1956, 1963; Gray and Jordan 2000). Blust (1988) also analyzed the words and phrases of Austronesian speakers and estimated the possible development of the Austronesian language family. His results show that the separation of Formosan (i.e., the

Taiwanese Austronesian languages) and Malayo-Polynesian may have occurred somewhere around Taiwan at around 4500 B.C. Therefore, Taiwan is the origin, or at least very close to the origin, of the Austronesian language family. Other research including linguistics, archaeology, and genetics also support this theory (Bellwood 1988; Diamond 2000; Melton *et al.* 1995, 1998; Trejaut *et al.* 2005). According to Bellwood (1988), the proto-Austronesians were an agricultural population living in coastal southeast China during the Neolithic period. Archaeological evidence such as the exchange of Taiwanese jade, pottery, and some other artifacts also support this assumption (Bellwood 1988, 1991; Bellwood and Dizon 2005; Hung *et al.* 2006; Tsang 2012). Bellwood (1987) suggests that a special kind of red-slipped pottery can be found in Taiwan, the Philippines and Pacific Islands. Based on typology and chronology, Bellwood (1987) concluded that this kind of red-slipped pottery most likely originated in Taiwan and dispersed with the Austronesians. Moreover, Bellwood and Dizon (2005) found pottery and stone tools with Taiwanese components in the Batanes Islands. Furthermore, they concluded that Taiwanese jade found in this area supports the hypothesis of movement out of Taiwan.

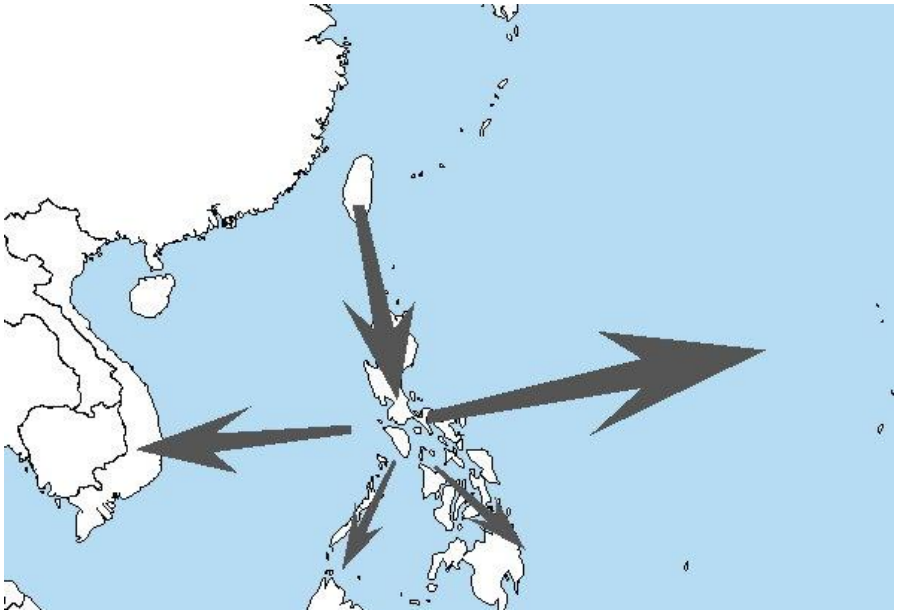

Figure 2.3. General dispersal pattern of the "Out of Taiwan" theory.

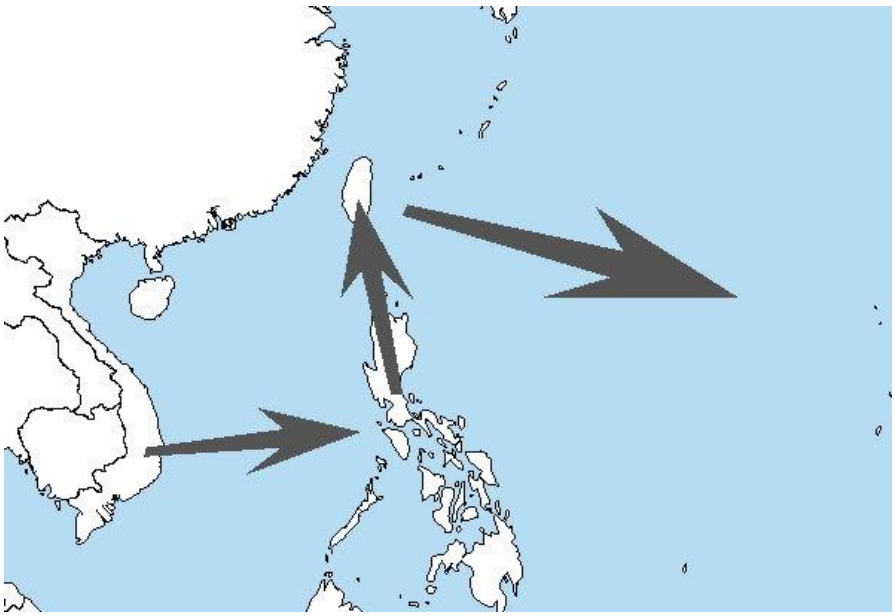

Figure 2.4. General dispersal pattern of the "Southeast Asia" theory.

The other major theory suggests that the homeland is somewhere in Southeast Asia (Figure 2.4). Scholars such as Oppenheimer and Richards (2001), Solheim (1988),

and Su *et al.* (2000) support this hypothesis. Solheim (1988) also used pottery evidence to support his "out of Southeast Asia" hypothesis. He suggested that the red-slipped pottery, which Bellwood mentioned, actually showed the component of the pre-Sa Huyunh-Kalanay pottery, one of the oldest types of pottery in Southeast Asia. Therefore, instead of originating in Taiwan, the red-slipped pottery actually came from Southeast Asia. He also pointed out difficulties in traveling from Taiwan to Philippines. In fact, he suggested that a reverse direction would be relatively easier due to ocean currents. Solheim (1988) further suggested that groups from southern Philippines and northeastern Indonesia spoke "pre-Austronesian" during the Pleistocene. Around 5000 B.C., these groups started to expand to the region to the north of Luzon (the chief island of the Philippines), southeast coastal China, and Taiwan around 4500 B.C.

Instead of linguistic and archaeological evidence, recent scholars also tried to approach this topic from a genetic perspective. Su *et al.* (2000) examine the Y-chromosome from 36 groups living in Southeast Asia, Taiwan, Micronesia, Melanesia, and Polynesia, examining their biological affinities. According to their research, none of the Taiwanese Y haplotypes were found in Micronesia and Polynesia. In fact, the results seem to suggest that there are two major routes: one to Taiwan and the other to Melanesia and then to Polynesia. In other words, the results from Y-chromosome analysis suggest that Taiwan is not the origin of the Polynesians, and that multiple routes are more likely.

However, the results from mtDNA analysis present a totally different conclusion (Melton *et al.* 1995, 1998; Mirabal *et al.* 2013; Trejaut *et al.* 2005). Trejaut *et al.* (2005) assessed mtDNA variation in 640 individuals from nine tribes of the Taiwanese

Indigenous. The results show that the haplogroup B4a1a is shared among the indigenous people of Taiwan, Melanesia, and Polynesia, which support the hypothesis that Taiwan may be the origin of these groups. In combining the results by Su *et al.* (2000), Trejaut *et al.* (2005) concluded that with the common element in mtDNA and the lack of common Y-chromosomal element between Taiwanese Indigenous and Polynesians, the proto-Oceanic societies would have been primarily matrilocal. Other research also supports the assumption that the maternal ancestry of Austronesian populations had an origin in Taiwan (Melton *et al.* 1995). Melton *et al.* (1995, 1998) used mtDNA and nuclear DNA to trace the homeland of the proto-Austronesians. In their research, four Taiwanese Indigenous groups (Amis, Atayal, Bunun and Paiwan) and 25 other groups from Asia and Oceania were analyzed. They found that the Taiwanese Indigenous appear to have been mostly isolated from mainland Asians for some unknown period of time, given a lack of sharing of contemporary control-region sequence. Moreover, the mtDNA SSO type (234), which can be found in every other East Asian population, is lacking among Taiwanese groups. In other words, they suggest that the Taiwanese Indigenous groups were generally separated from other Asian populations for a long time. However, there is some genetic similarity between the Taiwan populations and the people from the Philippines. Melton *et al.* (1995) concluded that this might due to migration from Taiwan to the Philippines. In general, their results support the assumption that the proto-Austronesians expanded to Taiwan from central or south China. Furthermore, the Taiwanese Indigenous groups originated from the same root instead of separate population settlements (Melton *et al.* 1998). A recent mtDNA study that used Neolithic

archaeological data also suggests that the early Austronesians arrived in the northern part of Taiwan around 6,000 years ago and then spread rapidly to the south. These people left Taiwan around 4,000 years ago, dispersing throughout island Southeast Asia, Madagascar, and Oceania (Ko *et al.* 2014).

Previous studies based on skeletal remains also provided some perspective. However, most of the earlier research was focused on univariate analysis methods. A series of studies (e.g., Hsu 1947; Kanasaki *et al.* 1947; Tsai 1950; Wang 1949; Wang 1950a, b; Wang 1950; Wu 1950a, b) done by earlier Japanese scholars and their students focused on basic osteometric data. For example, in Chang's (1949) research about Atayal, measurements and indexes were taken following Martin (1928) and compared individually. Furthermore, anthropometric and anthroposcopic studies were also popular (e.g., Chang 1947; Sheen 1949; Su 1950a, b, c.). For example, Chai (1967) provided detailed anthropometric and anthroposcopic information of the eight mountain indigenous groups. It is also noted that multivariate analysis methods were applied in Chia (1967) by using anthropometric data to calculate the Mahalanobis' generalized distance.

On the other hand, recent studies (e.g., Katayama and Doi 2008; Pietrusewsky 1995; Pietrusewsky and Chang 2003) approached the question of biological relationship among Taiwanese Indigenous groups using multivariate statistical analysis.

Pietrusewsky (1995) focused on the relationship between the Atayal and the other groups in Asia using craniometric data. Analyses using raw data and standardized data were conducted. The results showed that the Atayal clustered with the Chinese and that

the Atayal had little relation to Polynesian and other Oceanic groups. Moreover, in the analysis using standardized data, the Atayal had a closer relationship with the samples from Southeast Asia. In other words, these results seem to reject the assumption of the out of Taiwan model.

Pietrusewsky and Chang (2003) also analyzed the crania of five Taiwanese Indigenous groups (Atayal, Bunun, Pazeh, Babuza and archaeological remains from the Shi San Hang site) and 55 other cranial series. Their results show that the Babuza, Pazeh and Shi San Hang samples had a relatively closer relationship with each other, while the Atayal and Bunun represent another branch. They also found that there is a relatively strong relationship between the Taiwanese Indigenous and the samples from Polynesia. In other words, their research tends to support the hypothesis that Taiwanese Indigenous groups are the ancestors of the people of Remote Oceania. There is also a connection between the Taiwanese Indigenous groups and the samples from Southeast Asia analyzed by Pietrusewsky and Chang (2003). However, the direction of the migration is not clear. Pietrusewsky and Chang (2003) also found the affinity between some Taiwanese Indigenous groups (Bunun, Babuza, and Pazeh) and populations from northeastern and eastern Asia. In other words, their results suggest that the source of the Taiwanese Indigenous may be Northeast and East Asia.

Katayama and Doi (2008) used 6 cranial measurements of a female individual from Kenting-liao site, which is located at the southern part of Taiwan and has an occupation history of approximately 4500-3500 B.P., and compared it with five specimens from Tuvalu, Taumako, Mangaia, Mana and Okinawa. Nine mandibular

measurements were also used as variables in comparing the biological affinity between the six specimens. The results deriving from the cranial measurements and mandibular measurements did not agree with each other. Due to the small sample size and variables used, no further conclusions can be made from their analysis.

Recent Neolithic archaeological data were also used in tracing the diaspora of Taiwanese groups. Lauer (2015) analyzed samples from Neolithic Taiwan and China with a model-based R-matrix approach. He concluded that during Neolithic, cross-Taiwan Strait relationships were weak, which suggests that the Neolithic Taiwanese samples may not merely be the migrants from the west side of the Taiwan Strait. He also pointed out that Neolithic Taiwan had little connection with the Neolithic Chinese groups from the central river valleys in the north, which is likely due to restricted gene flow and cultural practices that limited the movement of genes. Furthermore, the general Neolithic Taiwan groups were isolated from the larger Chinese gene flow patterns. On the other hand, because of its geographic location, the results also show that Taiwan Strait area is at the root of the connections between China and Island Southeast Asia. Lauer (2015) suggested that the Neolithic Taiwanese may have been influenced by minimal, but long term gene flow from the Island Southeast Asia. Therefore, with time, the connection between Taiwan and mainland East Asia became weaker, while connections with Island Southeast Asian became stronger. As for the modern Taiwanese Indigenous groups, Lauer (2015) provided a diagram of the relationship of 30 groups based on Mahalanobis' generalized distance using 12 cranial measurements. It is noted that the Bunun clustered with Pazeh, and that the Atayal were generally in another cluster.

CHAPTER 3: BIODISTANCE

There is a long history of using quantitative and qualitative morphological features of the human skeleton in physical anthropology for investigating population structure and the relationships of the populations (Pietrusewsky 2008). Measures of relatedness or differences among groups are referred to as biological distance, or biodistance. The estimation of biodistance provides a way to examine how close or divergent populations are with each other using polygenic traits (Buikstra *et al.* 1990). Variation in skeletal morphology reflects genetic relatedness between populations. Individuals or populations that are more similar in skeletal morphology are considered to be biologically related. Furthermore, multiple scholars suggest that through biodistance studies, patterns of gene flow, population origins, and long-distance migration may be examined (Buikstra *et al.* 1990; Larsen 2015; Pietrusewsky 2014; Relethford and Blangero 1990; Smith 2011; Stojanowski and Schillaci 2006). Therefore, by comparing the similarities or dissimilarities of the human remains, aspects of population history may be examined.

Konigsberg (2006) traced the development of biodistance studies since the 1960s. He pointed out that in the early days of biodistance studies, influenced by the general trend in archaeology, researchers in the 1970s tried to examine the development of culture. For example, physical anthropologists examined whether culture was formed *in situ* or introduced through migration. Another research topic that often uses biodistance analysis is migration. For example, Lane and Sublett (1972) used biodistance analysis to estimate the mating/postmarital residence pattern of a historical cemetery in Pennsylvania.

The basic assumption of this kind of study is that since one sex would move after marriage, the biodistance of each sex should present a different pattern, homogeneous or heterogeneous. In the recent studies of biodistance, with the addition of the concept of population genetic theory, biodistance studies can further be developed into different kinds of models. For example, the Relethford-Blangero model that built upon Harpending and Ward (1982) is widely used in many studies (e.g., Nystrom 2006).

Buikstra *et al.* (1990) also reviewed the trends of biodistance studies that were published in the *American Journal of Physical Anthropology* between 1955 and 1985. Although there is a decreasing trend in the number of publications related to biodistance studies due to the rise of other fields, a wide variety of studies about biodistance were carried out nonetheless. The analytical type of studies which are categorized by Buikstra *et al.* (1990) as mainly focusing on specific groups can be further divided into topics including: inter-race (focusing on relatedness between continental groupings), inter-population (mainly addressing the origins of populations), intra-regional (focusing on the temporal or geographical continuity or differences in populations), and intra-site (diachronic changes of the population or kinship related topics). In conclusion, the biodistance studies were used as an important method for addressing population history and structure. Furthermore, according to the analysis of Buikstra *et al.* (1990), numerous papers about the methodology of biodistance studies have been published, which strengthen the foundation of biodistance studies.

For recent development in biodistance studies, inter-population and intra-regional studies still represent an important component for growth. These include studies such as

tracing the transition to Agriculture in Europe (e.g., von Cramon-Taubadel and Pinhasi 2011) or Japan (e.g., Pietrusewsky 2013), and tracing the population continuity (e.g., Godde 2010, 2013 about Nubians in lower Nubia). On the other hand, new studies such as applying the techniques and methods in tracing the origin and dispersal of modern *Homo* and identifying new hominin species are also popular (Pietrusewsky 2014). Furthermore, computer programs such as *FORDISC 3.1.307* (Jantz and Ousley 2005) and *CRANID* (Wright 2012), which are based on biodistance theories, are also widely used in forensic settings. As for methodology, the influences of climate and environmental factors remain a significant factor in biodistance studies (Pietrusewsky 2014). However, a new trend has emerged, giving special focus to identifying which elements had the strongest correlation with biological affinity (Pietrusewsky 2014).

An underlying assumption of biodistance studies is that populations which exchange genes will become more similar, thus resulting in phenotypic similarities. The similarity or dissimilarity of human remains can be described by either quantitative (metric) or qualitative (non-metric) methods. In other words, cranial variation reflects genetic variation (von Cramon-Taubadel and Weaver 2009). Quantitative data are recorded by measuring distances or angles between anatomical landmarks. The benefits of using metric data (especially craniometric) vary (Pietrusewsky 2008). The results of measurements are relatively more precise and reliable. Since there is a long history of the use of craniometric data in anthropology, standardized measurements and landmarks are provided (e.g., Bookstein 1997; Buikstra and Ubelaker 1994:69-78; Howells 1973, 1989; Martin 1928; Martin and Saller 1957; Moore-Jansen *et al.* 1994; Ousley and McKeown

2001). Moreover, various publications and databases (e.g., Howells 1996) are now available for use. Qualitative data are recorded by observing the presence or absence of non-metric traits. Unlike metric data that normally require a complete set of remains, in cases where the preservation conditions are poor, non-metric traits can sometimes still be recorded. In the present study, both quantitative and qualitative data were recorded for analysis.

Prior to a discussion about quantitative or qualitative data, it is necessary to explain how these traits (variables) reflect genetic relationships, or heritability. Heritability (h^2) is defined as $h^2=V_a/V_p$, where V_a is the additive genetic variance and V_p is the phenotype variance (Carson 2006a, b). Therefore, heritability can be understood as a measurement of how much variation in a phenotypic trait in a certain population is determined by genetics (Carson 2006a, b; Falconer and MacKay 1996). The value of heritability (h^2) can range from 0.0 to 1.0; a high value of heritability indicates that the expression of the trait is highly influenced by genetics. For example, a value of 1.0 heritability indicates that the expression of the trait is completely under genetic control. However, it is noted that these polygenic traits contain both environmental and genetic factors (Buikstra *et al.* 1990; Relethford and Lees 1982), i.e., it must be kept in mind that biodistance may reflect both environmental and genetic differences between populations.

Previous research suggests that in human populations, craniofacial variation can reflect the underlying genetic pattern (Buikstra *et al.* 1990; Cheverud 1988; Konigsberg 2006). Several studies have focused on the heritability of craniometric traits through twin studies; for example Dahlberg (1926), Vandenberg (1962) and Sharma *et al.* (1984).

Recent studies of the heritability of craniometric traits include: Carson (2006a), Martinez-Abadias *et al.* (2009), Sjøvold (1984), and Sparks and Jantz (2002). In general, Carson (2006a) and Sjøvold (1984) concluded that most of the measurements showed significant heritability and those measurements, which are related to the size of the brain, orbits, nasal area, and oral areas, had a relatively higher heritability rate. Multiple studies (Harvati and Weaver 2006a, b; Smith 2009; Smith *et al.* 2007; von Cramon-Taubadel 2009) also suggested that the shape of the temporal bone is one of the most reliable indicators of past population history, along with the sphenoid, frontal, and parietals.

On the other hand, Martinez-Abadias *et al.* (2009) suggested that though the values of heritability of craniometric traits were substantial, there were no statistically significant differences among the heritability of facial, neurocranial and basal dimensions. Though the value of heritability varies in different studies, the common practice in human craniometric studies is to apply an average estimated heritability (h^2=0.55), or assume that the trait is fully controlled by genetics (h^2=1.0) (Carson 2006a; Cheverud 1988).

For non-metric traits, studies that use human samples for heritability were limited due to the lack of sufficient sample sizes (Carson 2006b). Sjøvold (1984) examined the heritabilities of multiple non-metric traits. The results showed that many non-metric traits had relatively high heritability. On the other hand, Carson (2006b), who used the same sample, suggested that most of the heritabilities do not differ significantly from a model of h^2=0. However, despite the low heritability values estimated by Carson (2006b), multiple studies through different approaches, including animal studies, suggested that many of the non-metric traits were genetically controlled (reviewed in Berry and Berry

1967; Cheverud and Buikstra 1981a, b, 1982; Grüneberg 1963; Hauser and De Stefano 1989; Leamy 1974; McGrath *et al.* 1984; Richtsmeier and McGrath 1986). Moreover, according to Godde (2013) and Stefan and Chapman (2003), the results that utilized non-metric traits showed similar conclusions as metric data. Multiple studies also suggested that the results of non-metric traits showed similar results as those based on classic genetic markers (Hanihara 2008; Hanihara *et al.* 2003; Movsesian 2005). Furthermore, Ricaut *et al.* (2010) concluded that non-metric traits are correlated with genetics. Based on the discussion above, although non-metric traits may be inferior to metric traits, they can still be of value in biodistance studies.

Other than heritablility, it is also important to mention that cranial variation showed a strong geographic pattern (Pietrusewsky 2014). Howells (1973) first provided a global study with cranial series from around the world. The results show that cranial variation is geographically structured, with a high level of accuracy in classification. Further studies (e.g., Relethford 2001, 2002) have also shown geographic patterning based on cranial variations. Moreover, studies based on non-metric cranial variation (e.g., Hanihara 2008; Hanihara and Ishida 2001a, b, c, d) also show geographic patterning. In general, the studies show that there is a close correspondence between geographic distance and phenotypic distance in human populations (Relethford 2004a, 2009, 2010). Although some studies (e.g., Hubbe *et al.* 2009; Relethford 2004a, b; Roseman 2004) suggested that some aspects of cranial morphology are correlated with climate, they also point out that, on average, the signal from population history can still be detected. Furthermore, though previous studies (e.g., Cavalli-Sforza *et al.* 1994; Eller 1999;

Roseman and Weaver 2004; Strauss and Hubbe 2010; Smith 2009; von Cramon-Taubadel 2009) have shown correspondence between patterns of craniometric variation and neutral models of population structures, it is important to note that craniometric variation is not completely neutral. As Relethford (2010) summarized and concluded: "selection will sometimes act to obscure, but not erase the signature of population history and structure." Therefore, multivariate statistical analysis of cranial variation can be used as a powerful method to construct population history and structure.

Quantitative Data

As mentioned in Chapter 2, few studies have used a multivariate analysis method when approaching the question of biological relationships among Taiwanese Indigenous populations. However, the use of multivariate statistical procedures in biodistance studies is widespread in other areas. Several scholars have reviewed and summarized their application (Buikstra *et al.* 1990; Howells 1969, 1973, 1989; Konigsberg 1990; Larsen 2002, 2015; Relethford and Lees 1982). According to Pietrusewsky (2008), who reviewed the use of multivariate statistical procedures for analyzing metric data, multivariate statistical procedures are powerful for examining the relationships among variables and group differences. Furthermore, as concluded by Howells (1969, 1973), multivariate analysis allows for the cranium to be treated as a complete unit and for the relationship of the variables to be taken into account. Relethford and Lees (1982) also pointed out that mathematically, multivariate analysis approaches avoid the problem of type-I errors which commonly occur in univariate analysis.

Relethford and Lees (1982) reviewed two approaches in biodistance studies that use quantitative traits: the model-free and model-bound approaches. According to them, the model-free approach does not apply the models of population structure. Therefore, population parameters such as the proportion of admixture and kinship coefficients are not estimated in the model-free approaches. The model-bound approaches, on the other hand, use population structure models. Specific population parameters are estimated during the analysis. Pietrusewsky (2014) further summarized that model-free approaches focused more on the overall similarity among groups, while model-bound approaches required more assumptions and allowed for the estimation of microevolutionary processes (e.g., gene flow or genetic drift). Model-bound approaches required more assumptions with the goal of estimating a specific parameter, while model-free approaches dealt with overall similarity (Relethford and Lees 1982). In the present research, a model-free approach is used.

Two of the most common statistical procedures for analyzing metric data are discriminant function analysis and the Mahalanobis' generalized distance (Howells 1969, 1973; Jantz 1973; Relethford and Lees 1982; Pietrusewsky 2008). According to Pietrusewsky (2008), the purpose of discriminate function analysis is to maximize the differences between two or more groups through a series of combinations of variables. Although discriminant function analysis was originally used to classify an unknown individual specimen into one or sometimes more groups, Campbell (1978) pointed out that this method is also useful for measuring how distant groups are. Furthermore, in

addition to describing group separation, discriminant function analysis can also identify the relative contribution of variables to differentiate groups (Rencher 2002).

Theoretically, distance can be measured in a variety of ways, one of the simplest being is the Euclidean distance, which is:

$$\sqrt{(X_1 - Y_1)^2 + (X_2 - Y_2)^2 + \cdots (X_n - Y_n)^2}$$

where $\{X_1, X_2, \ldots, X_n\}$ and $\{Y_1, Y_2, \ldots, Y_n\}$ represent the coordinates of two points where n variables are used. However, in the study of biodistance, Mahalanobis' generalized distance is commonly used in place of the Euclidean distance (Howells 1973; Konigsberg 2006; Pietrusewsky 2008). Mahalanobis' generalized distance was first created by Mahalanobis (Mahalanobis 1927, 1930, 1936; Mahalanobis *et al.* 1949). The original use of Mahalanobis' generalized distance was to compare crania from India using craniometric data.

However, similar to the traditional Euclidean distance, Mahalanobis' generalized distance takes the correlations of the data sets into consideration, i.e., the covariance matrix is considered. The formula of Mahalanobis' generalized distance can be written as:

$$D^2 = (X - Y)'S^{-1}(X - Y)$$

where X and Y are the matrix of $\{X_1, X_2, \ldots, X_n\}$ and $\{Y_1, Y_2, \ldots, Y_n\}$, and S is the covariant matrix (Mahalanobis 1936; Rencher 2002). When the covariance matrix (S) is a unit matrix, Mahalanobis' generalized distance is equal to Euclidean distance.

According to Pietrusewsky (2008), Mahalanobis' generalized distance can be understood as a calculation that used the pooled within-group variance to maximize the

difference between pairs of groups, which are contributed by the inserted inversed covariance matrix. The use of the inversed covariance matrix may help to eliminate correlations between the variables and also serve to standardize the variables to the same variance (Mahalanobis 1936; Rencher 2002). Therefore, in general, Mahalanobis' generalized distance may be suitable for detecting similarity and dissimilarity between groups. As Keita and Boyce (2008) mentioned, Mahalanobis' generalized distance can be considered a measure of dissimilarity, since a large value indicates less affinity.

In conclusion, the use of discriminant function analysis and Mahalanobis' generalized distance are used in the present research to separate groups and measure the distance between the centroids of these groups.

Qualitative Data

Qualitative data are recorded as the presence or the absence of a trait. More specifically, the presence of a trait is due to a series of inherited genes and the environmental pressures that push the trait past the threshold of expression (Cheverud and Buikstra 1981b; Falconer 1989; Hauser and De Stefano 1989).

The history of the use of non-metric traits is discussed in Saunders and Rainey (2008). Starting in the 19th century, interest in descriptive morphology and embryology led to the discovery of many non-metric traits in the human skeleton. Mendel's principle further creates a foundation for using these traits to describe population variation. Hooton (1920, 1925, 1930) provides some of the earliest works with detailed trait lists and sorts these observed traits by population. During the 1950s and 1960s, with the rise

of genetic studies, researchers investigated the characteristics of non-metric traits through genetic studies of mice (*Mus musculus*). Grüneberg (1952) described the distribution of non-metric traits as quasi-continuous, which simply suggests the effect of thresholds. This research opens the discussion for the influence of environmental factors. Howe and Parsons' (1967) work based on mice found that when calculating the divergence based on combining the observation of 25 non-metric traits, the physiologic and environmental factors did not show a significant influence. In other words, this research showed that biodistance analysis using non-metric traits is legitimate when a large number of traits are employed. Furthermore, Berry and Berry (1967) arrived at a similar conclusion when they analyzed non-metric traits in humans, which caused biodistance studies utilizing non-metric traits to multiply. Detailed descriptions of 30 non-metric traits were also described in their study, which were commonly used in later studies. Berry (1974) also provided a verification of the use of non-metric traits. A total of 30 non-metric traits from 21 spatially distinct samples were used to estimate biodistance between groups. The results were in agreement with the historical record, which indicates that non-metric traits can be useful in reflecting genetic information.

Berry and Berry (1967) suggested that most of these non-metric traits are genetically determined. Therefore, analysis of the frequency of these traits can reflect the genetic affinity between groups. The application of non-metric data was widely used in both archaeological and modern contexts (e.g., Berry 1974; Berry and Berry 1967; Buikstra 1980; Donlon 2000; Godde 2010, 2013; Edger 2007, 2009; Hanihara 2008; Hanihara *et al.* 2003, 2012; Hefner 2009; Irish 2010; Irish and Konigsberg 2007;

Konigsberg 1990; Lane and Sublett 1972; Matsumura and Oxenham 2013; Myagmar 2013; Ossenberg 1976; Ossenberg *et al.* 2006; Pietrusewsky 1970, 1971, 1977, 1984). For example, Godde (2010) examined the identity of the Meroites in lower Nubia and whether they were different from or descendants of the Nubians that previously occupied this area. A total of 11 traits were used in the analysis. The results showed that, when compared with six different groups, the Meroites had a closer relationship with other Nubians. In other words, their study supported the hypothesis that the Meroites were the descendants of the Nubians that once occupied this area.

Though non-metric traits were successfully used, there are several issues that need to be considered when applying this kind of variation. Since non-metric traits cannot be measured, the data were recorded by observing the presence or absence of the trait. However, for bilateral traits (i.e., traits that occur on both the left and right sides such as the parietal notch), the frequency calculation would need to be used with caution. Some researchers (including Harris and Sjøvold 2004) suggested that bilateral traits should be counted separately, which in turn increases the sample size. While numerous studies pointed out that there is a strong correlation between bilateral traits and that they are more likely to be controlled by the same genes, asymmetry is present due to incomplete penetrance during ontogenesis (Cesnys 1982; Korey 1980; McGrath *et al.* 1984; Perizonius 1979).

Two different methods were commonly used for calculating biological distance using non-metric traits: Mean Measure of Divergence (MMD) and the modified Mahalanobis' generalized distance (D^2). Mahalanobis' generalized distance, as explained

earlier, can also be used with non-metric data. Konigsberg (1990) extended the covariant matrix by using a tetrachoric correlation matrix for the categorical data. Since the non-metric traits were scored dichotomously, the tetrachoric correlation coefficient may thus be used. The modified Mahalanobis' generalized distance formula by Konigsberg (1990) is:

$$D_{ij}^2 = (z_{ik} - z_{jk})' T^{-1} (z_{ik} - z_{jk})$$

where z_{ik} and z_{jk} are the threshold values corresponding to trait frequency of trait k of group i and j, and T is a pooled with-in group tetrachoric correlation matrix between the traits.

Compared to this relatively new method, MMD has been used for a long time. The MMD was originally introduced by C. A. B. Smith and used in Grewal (1962) for the estimation of biological divergence in mice. Berry and Berry (1967) subsequently applied this method to human cranial samples. A great many studies subsequently were carried out by applying the MMD to cranial, postcranial, and dental non-metric traits (e.g., Berry 1974; Berry and Berry, 1967; Buikstra 1980; Donlon 2000; Edger 2007, 2009; Godde 2010, 2013; Hanihara 2008; Hanihara *et al.* 2003, 2012; Hefner 2009; Irish 2010; Irish and Konigsberg 2007; Konigsberg 1990; Lane and Sublett 1972; Matsumura and Oxenham 2013; Myagmar 2013; Ossenberg 1976; Ossenberg *et al.* 2006; Pietrusewsky 1970, 1971, 1977, 1984).

In regard to which method is appropriate, several scholars suggest that the modified Mahalanobis' generalized distance (D^2) should be selected instead of the MMD (e.g., Godde 2010, 2013; Kongsberg 2006; Schillaci *et al.* 2009). However, according to

Irish (2010) and Nikita (2015), the results from MMD are highly correlated with the modified Mahalanobis' generalized distance. Nikita (2015) also pointed out that the MMD has the advantage of being an unbiased estimator. Furthermore, the MMD only requires summary count data; thus, in cases where there is much missing data, the MMD can still be used (Irish 2010), allowing an easier comparison with other data. Therefore, in the present study the calculation of MMD was used for analyzing the qualitative data.

CHAPTER 4: MATERIAL AND METHODS

Samples

A total of 165 adult crania representing both males and females from four Taiwanese Indigenous populations (Atayal [n=45], Bunun [n=40], Babuza [n=43], and Pazeh [n=37]; Figure 4.1; Table 4.1) were sampled. These crania are curated in the collection of the Graduate Institute of Anatomy and Cell Biology, National Taiwan University, Taipei, Taiwan were analyzed. The collection was compiled during the Japanese colonial period (1890s-1950s). Most of the skeletons came from the cemetery of the tribe or victims of the rebellion collected by the Japanese scholars under the authorization of the colonial government.

Table 4.1. NTU samples used in the present study.

Sample	No. of crania (Female/Male)	Notes
Atayal	45 (15/30)	NTU; collected by author
Bunun	40 (16/24)	NTU; collected by author
Babuza	43 (19/24)	NTU; collected by author
Pazeh	37 (15/22)	NTU; collected by author
Total	**165(65/100)**	

As mentioned previously, accurate information of the tribe affiliation of the sample is important. Though Turner and Lien (1984) warned that Taiwanese Indigenous groups may have been influenced by later immigrants from the Chinese mainland around 4000 to 1000 BP, it is still necessary to use a modern sample. As mentioned, many of the previous studies about the dispersal of the Austronesian-speaking people or Taiwanese

Indigenous were either linguistically or ethnographically based. In other words, they are based upon modern or relatively recent samples. Since the connection between archaeological sites and a certain tribe may not be clear, using a modern sample may be necessary.

Again, as mentioned, the most significant challenges of using modern samples include the increased mixing and the influence of government force during the recent decades (see Chapter 1). However, due to the special historical context of how the collection was built, the collection from the National Taiwan University (NTU) minimized these impacts and therefore may be the best and only material available to examine the biological affinity of Taiwanese Indigenous. It is also noted that a reorganization project of the NTU collection was started around 1997 (Tsai 2009, pers. comm.; Lu pers. comm.). During this project the curators found that some of the provenience information and the specimen labels were misplaced. Therefore, special attention must be paid for future studies.

Sex of each cranium was estimated using the criteria described by Buikstra and Ubelaker (1994:19-21). The criteria include: mastoid processes, supraorbital margins, glabella, nuchal crest, and mental eminence. Walker's (2008) spreadsheet was used to provide final estimation. Detailed age-at-death information is not presented in the present study. However, all specimens are adult crania based on the complete fusion of the spheno-occipital synchondrosis and fully developed third molars.

The Atayal group is the most widespread and second largest mountain indigenous group in Taiwan (Wei and Wang 1966). The crania in the present study are all from the

same location at the southern edge of their territory, which is at the northern part of Nantou. Most of the crania were collected by Dr. Kanaseki and his students from the victims of the Wushei incident, a fight between the Taiwanese Indigenous tribes with the Japanese colonial government in 1930 (Howells 1989:109; Tsai, pers. comm.). It is noted that in 2008, the Seediq group, believed to be the major group, participated in the Wushe incident, and was separate from the Atayal group. However, in the present study, the older division method (i.e., no separation of the Seediq group from the Atayal population) is considered due to various reasons. First of all, the general language and cultural system of the two groups were very similar (Lee 2011; Kano 1955; Sayama 1913-1921). Previous scholars claimed that their similarities in biology and culture support that they were the same group, while any differences were due to separation in living location (Kano 1955; Kojima 1915-1921; Sayama 1913-1921). Moreover, since the collection was made by the Japanese scholars who followed the previous division method, the provenience information did not separate the two groups. Therefore, in the present study, a bigger Atayal sample which includes both Seediq and Atayal is used in this study.

The Bunun population is the fourth largest and the second-most widespread mountain indigenous group in Taiwan (Wei and Wang 1966). All crania used in the present study are from the same cemetery of the Bahoan tribe (Tsai, pers. comm.). The remains were collected by Dr. Tsai and his colleague from the late 1960s to 1970s. Though the location of the cemetery is now in the Hualian area, it is known that the

Bunun from Bahoan tribe originally lived in the Nantou area. The migration to the modern location occurred approximately 80 years ago (Cheng 2000; Tsai, pers. comm.).

The Babuza and Pazeh tribes are the lowland indigenous groups in the central west area of Taiwan. The Babuza crania used in this study were mostly from Hsilo, which is located west of the Nantou. The Pazeh crania used in this study are primarily from Wuniulan, the Puli basin of the Nantou area.

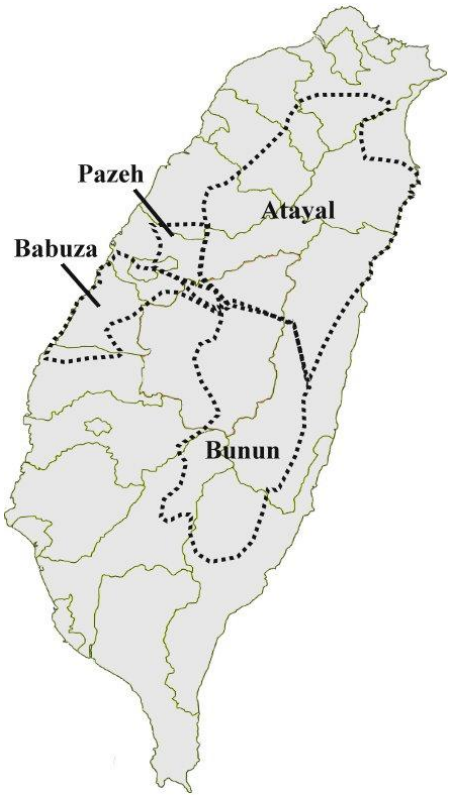

Figure 4.1. Location of the four indigenous groups, redrawn from Lee (2011: supplement).

Data from an additional four samples: South Japan (n=91; North Kyushu, recent inhabitants, Howells 1989), Philippines (n= 50; mainly from Manila; pre- World War II, Howells 1989), and Hainan (n= 83; Chinese; recent inhabitants, Howells 1989) from the

Howells' (1996) World Craniometric Data Set were also used for comparison (Table 4.2, Figure 4.2). It is noted that though the Atayal sample is available in the Howells' data set, it was not used in the present analysis. It was excluded in order to avoid potential duplication, since some of the data from Howells' data set were collected from the NTU collection (Howells 1989), and specimens were exchanged between the Academia Sinica and the NTU previously (Tsai, pers. comm.).

Figure 4.2. Samples used for craniometric analysis.

For the non-metric analysis, four additional samples were used: Okinawa (n=131; recent inhabitants), Philippines (n=230; recent native inhabitants), south Chinese (n=91; Yangtze River area), and mainland Southeast Asians (n=294; recent inhabitants), summarized in Fukumine *et al.* (2006) (Table 4.3, Figure 4.3). The comparative samples are from neighboring regions of Taiwan.

Figure 4.3. Samples used for non-metric traits analysis.

Sample Screening

Before samples were used for the biodistance analysis, some crania had to be eliminated through visual observation by the author. Crania with evidence of perimortem trauma or postmortem modification were eliminated from the analysis (e.g., perimortem chop marks on the associated mandible). This is due to traditions of head hunting in many Taiwanese Indigenous groups (Kojima 1915-1921; Mori 1912; Sayama 1913-1921). For example, in the Bunun tribe, the head hunting practice is called *kanasan*, and in Atayal tradition the hunted head would be placed on a shelf called *sakaw tunux*, meaning "the bed for head." Since the trophy heads are mostly from external groups, crania with potential evidence of head hunting behavior were removed from the present study. The preservation status of the crania was also considered before further analysis. Fragmented crania were eliminated due to the amount of data that would be missing during analysis.

As for craniometrics, crania with any of the following areas damaged were removed from the analysis: prosthion, glabella, bregma, lambda, opisthion, basion, and the nasal area.

Therefore, the final number of crania used in the craniometric analysis is 335, and the number of crania used in the non-metric trait analysis is 895 (Table 4.2 and 4.3).

Table 4.2. Samples used for craniometric analysis.

Sample	No. of crania (Female/Male)	Notes
Atayal	34 (13/21)	NTU; collected by author
Bunun	24 (7/17)	NTU; collected by author
Babuza	30 (12/18)	NTU; collected by author
Pazeh	23 (9/14)	NTU; collected by author
South Japan	91 (41/50)	From Howells' (1996) data set
Hainan	83 (38/45)	From Howells' (1996) data set
Philippines	50 (0/50)	From Howells' (1996) data set
Total	**335 (120/215)**	

Table 4.3. Samples used for non-metric analysis.

Sample	No. of crania (Female/Male)	Notes
Atayal	36 (13/23)	NTU; collected by author
Bunun	40 (16/24)	NTU; collected by author
Babuza	39 (18/21)	NTU; collected by author
Pazeh	33 (13/20)	NTU; collected by author
Okinawa	131 (sexes are pooled)	From Fukumine *et al.* (2006)
Philippines	230 (sexes are pooled)	From Fukumine *et al.* (2006)
South Chinese	91 (sexes are pooled)	From Fukumine *et al.* (2006)
Mainland Southeast Asians	295 (sexes are pooled)	From Fukumine *et al.* (2006)
Total	**895**	

Recording of Data

Craniometric Data

The craniometric data were collected using a MicroScribe™ G2 digitizing system. The data were recorded as three-dimensional coordinates of points with an accuracy of 0.38 mm (Immersion Corporation 2002). The 3Skull program, developed by Ousley (2014) was used to record the specific points and craniometric landmarks and to calculate the measurements for further analysis.

The definitions of the craniometric landmarks and measurements were identified following the instructions of Howells (1973), with some exception defined by Martin (1928), Martin and Saller (1957), Ousley and McKeown (2001), and Weisensee and Jantz

(2011) (Table 4.4; Figures 4.4-4.6). The *FORDISC 3.1* help file (Jantz and Ousley 2005) was also used to assist in locating the landmarks. A total of 80 landmarks and two arcs were recorded for each cranium unless there was damage. Table 4.4 summarizes the landmarks and arcs that were recorded, with an illustration showing the position of each in Figures 4.4-4.6. It is noted that the occipital arc was not recorded due to the position of the crania during data recording. Moreover, landmarks that required instrumental assistance were marked with the help of calipers before digitizing. Furthermore, several landmarks were defined automatically by the 3Skull program (Ousley 2014) after recording the arc information.

Table 4.4. Summary of the landmarks recorded.

Landmark/ Arc	No. in Figures	Note
Prosthion- Howells	1	Howells 1973:169
Prosthion- Martin	2	Martin and Saller 1957:449
Subspinale	3	Howells 1973:170
Inferior nasal border	5, 6	Howells 1973:175
Alare	4, 7	Howells 1973:176
Nasale inferius	9, 10	Weisensee and Jantz 2011:550
Nasomaxillary suture pinch	12, 14	Howells 1973:179
Nasal bone elevation	13	Howells 1973:179
Deepest point on nasal bone profile	15	Howells 1973:178
Zygoorbitale	16, 17	Howells 1973:170
Lower orbital border	18	Left only; Howells 1973:175
Upper orbital border	19	Left only; Howells 1973:175
Cheek height sup. point	20	Left only; Howells 1973:180
Cheek height inf. point	21	Left only; Howells 1973:180
Ectoconchion	22, 25	Howells 1973:168
Dacryon	23, 24	Howells 1973:167
Zygion	26, 33	Howells 1973:173
Zygomaxillare	29, 30	Howells 1973:170
Zygotemporale inferior	31	Howells 1973:179
Zygotemporale superior	32	Weisensee and Jantz 2011:550

Table 4.4. Summary of the landmarks recorded.

Landmark/ Arc	No. in Figures	Note
Jugale	34, 51	Howells 1973:175
Marginal process lateral	35, 50	Ousley and McKeown 2001:179
Frontomalare temporale	36, 49	Martin and Saller 1957:451
Frontomalare anterior	37, 48	Howells 1973:168
Frontotemporale	38, 47	Martin 1928:618
Sphenion	39, (46)	Weisensee and Jantz 2011:550
Krotaphion	40, (45)	Ousley and McKeown 2001:179
Maximum frontal point	41, 44	Howells 1973:172
Stephanion	42, 43	Howells 1973:169
Nasion	52	Howells 1973:169
Glabella	53	Howells 1973:170
Supraglabellare	54	Howells 1973:181
Bregma	55	Howells 1973:167
Lambda	56	Howells 1973:168
Asterion	57, (68)	Howells 1973:166
Eurion	58, 67	Howells 1973:172
Radiometer point	59, (64)	Howells 1973:183
Porion	60, (65)	Howells 1973:176
Mastoideale	61, 66	Howells 1973:176
Radiculare	62, (63)	Howells 1973:173
Opisthion	69	Howells 1973:169
Basion	70	Howells 1973:166
FOB point	71, 72	Weisensee and Jantz 2011:550
Ectomolare	73, 75	Howells 1973:176
M1 anterior point	74	Howells 1973:184
Hormion	N/A	Weisensee and Jantz 2011:550
Alveolon	77	Martin and Saller 1957:451
Maximum malar projection point	102	Left only; Howells 1973:180
Metopion	103	Arc define; Howells 1973:181
Parietal subtense point	104	Arc define; Howells 1973:182
Vertex radius point	105	Arc define; Howells 1973:1883
Opisthocranion	106	Howells 1973:170
Nasale superius	108, 109	Weisensee and Jantz 2011:550
Frontal Arc	FRA	Howells 1973:186
Parietal Arc	PAA	Howells 1973:187

* numbers in brackets: right side, not shown in the figures

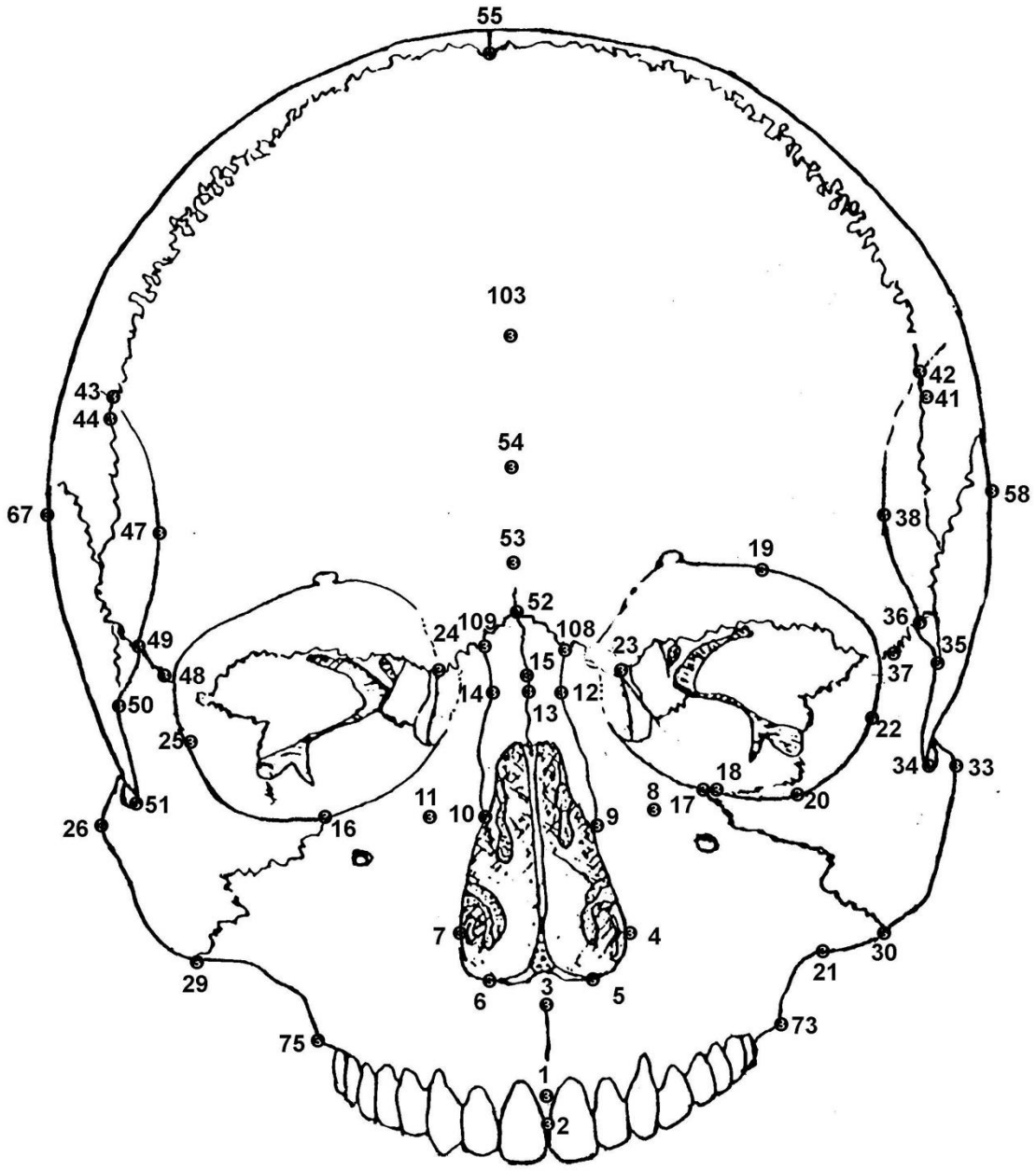

Figure 4.4. Anterior view of the craniometric landmarks (modified from 3Skull help file, Ousley 2014).

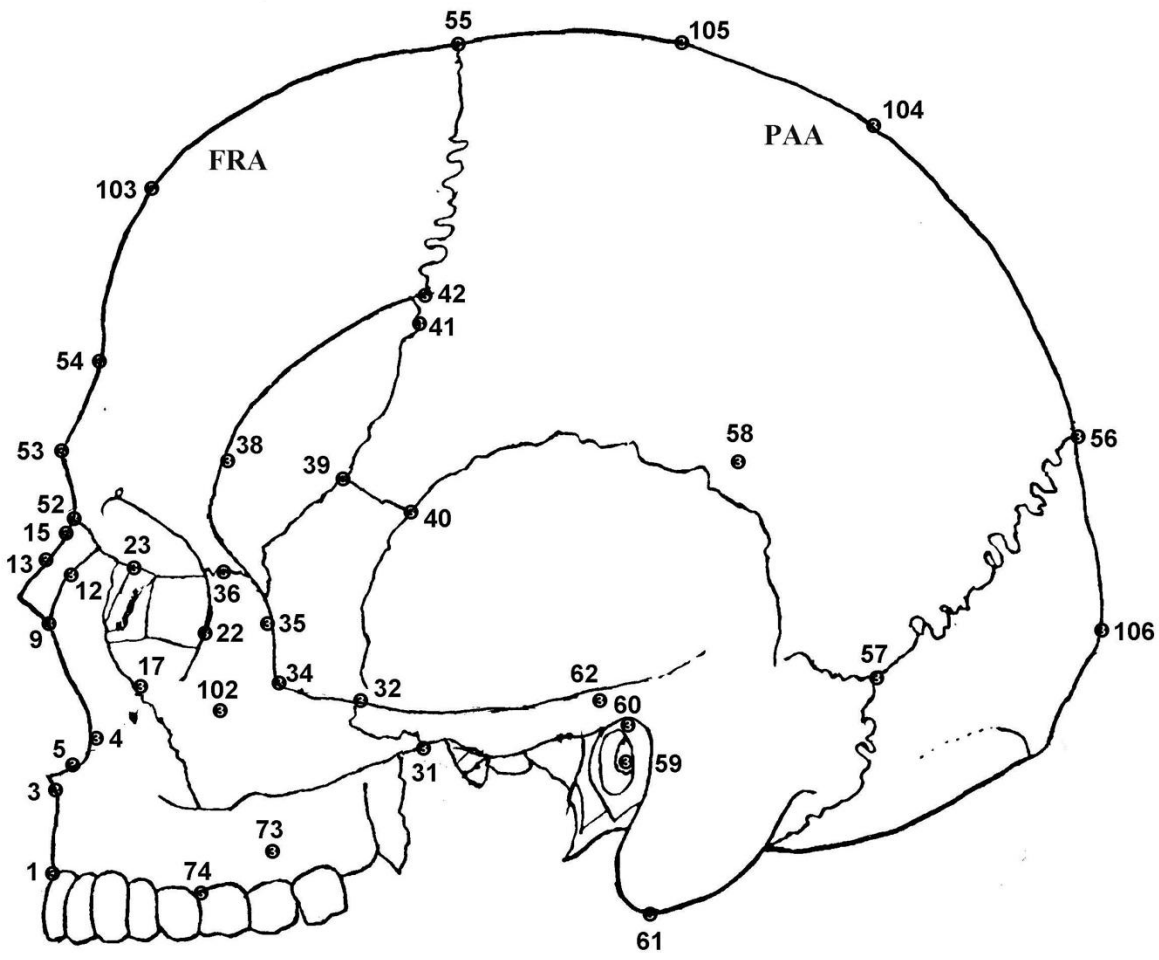

Figure 4.5. Lateral view (left side) of the craniometric landmarks (modified from 3Skull help file, Ousley 2014).

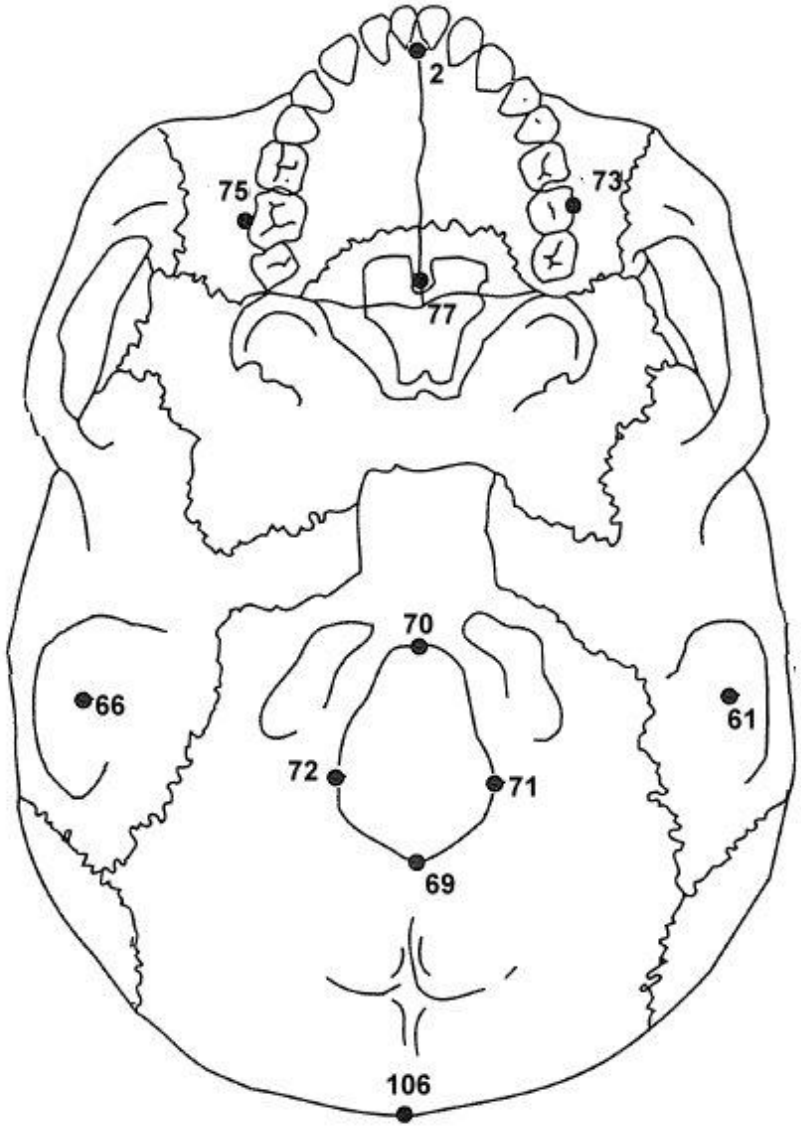

Figure 4.6. Inferior view of the craniometric landmarks (modified Buikstra and Ubelaker 1994:73).

A maximum of 107 measurements (including measurements from mandible) can be calculated from the 3Skull program (Ousley 2014). However, any measurement with more than 5 data points missing was removed from the analysis. Five more measurements were further removed due to lack of corresponding data in Howells' data set. Another eight measurements were removed due to lack of definition in

Howells (1989). Additionally, all measurements of angles were also removed. The total number of measurements used in this study is 40 (Table 4.5).

Table 4.5. Summary of the measurements used.

Abbr.	Measurement	Reference
GOL	Maximum Cranial Length	Howells (1973:170-171)
NOL	Nasio-occipital Length	Howells (1973:171)
BNL	Cranial Base Height	Howells (1973:171-172)
BBH	Basion-Bregma Height	Howells (1973:172)
XCB	Maximum Cranial Breadth	Howells (1973:172)
XFB	Maximum Frontal Breadth	Howells (1973:172)
ZYB	Bizygomatic Breadth	Howells (1973:173)
AUB	Biauricular Breadth	Howells (1973:173)
ASB	Biasterionic Breadth	Howells (1973:174)
BPL	Basion-Prosthion Length	Howells (1973:174)
NPH	Nasion-prosthion Height	Howells (1973:174)
NLH	Nasal Height	Howells (1973:175)
JUB	Bijugal Breadth	Howells (1973:175-176)
NLB	Nasal Breadth	Howells (1973:176)
MDH	Mastoid Height	Howells (1973:176-177)
OBH	Orbital Height	Howells (1973:175)
OBB	Orbital Breadth	Howells (1973:175)
DKB	Interorbital Breadth	Howells (1973:178)
NDS	Naso-dacryal Subtense	Howells (1973:178-179)
WNB	Simotic Chord (Least Nasal Breadth)	Howells (1973:179)
ZMB	Bimaxillary Breadth	Howells (1973:177)
FMB	Bifrontal Breadth	Howells (1973:177-178)
NAS	Nasio-frontal Subtense	Howells (1973:178)
EKB	Biorbital Breadth	Howells (1973:178)
DKS	Dacryon Subtense	Howells (1973:178)
IML	Malar Length, inferior	Howells (1973:179-180)
XML	Malar Length, maximum	Howells (1973:180)
WMH	Cheek Height	Howells (1973:180)
GLS	Glabella Projection	Howells (1973:181)
STB	Bistephanic Breadth	Howells (1973:173)

Table 4.5. Summary of the measurements used.

Abbr.	Measurement	Reference
FRC	Frontal Chord	Howells (1973:181)
PAC	Parietal Chord	Howells (1973:182)
NAR	Nasion Radius	Howells (1973:183)
SSR	Subspinale Radius	Howells (1973:183)
PRR	Prosthion Radius	Howells (1973:183)
DKR	Dacryon Radius	Howells (1973:183)
ZOR	Zugoorbitable Radius	Howells (1973:183)
FMR	Frontomalare Radius	Howells (1973:183)
EKR	Ectoconchion Radius	Howells (1973:184)
ZMR	Zygomaxillare Radius	Howells (1973:184)

Non-metric Data

Twenty cranial and mandibular non-metric traits (Table 4.6) were observed and recorded following the definitions from Hanihara and Ishida (2001a, b, c, d). The traits were selected in order to compare with the comparative data from Fukumine *et al.* (2006). Moreover, Hanihara and Ishida (2001a, b, c, d) suggested that there was a difference in the frequency of the traits among groups and that these traits were not influenced by sex, age, or intertrait correlations. Furthermore, many of the traits used in Hanihara and Ishida (2001a, b, c, d) have also been used in multiple studies (e.g., Berry and Berry 1967; Dodo 1974; Hauser and De Stefano 1989; Ossenberg 1970) and are influenced by the action of multiple genes. However, it is noted that most of the crania lacked a corresponding mandible; therefore, accessory mental foramen and mylohyoid bridging were removed from the analysis. Moreover, condylus tertius, jugular foramen bridging, and precondylar tubercle were also removed from the analysis due to the zero frequency

presence in all samples. The total number of non-metric traits used in the present study is 15. It is noted that several studies (e.g., DiBartolomeo 1979; Frayer 1988; Kennedy 1986; Standen *et al.*1997) suggested that the frequency of the presence of the auditory exostosis may be related with exposure to cold water. However, since this factor influenced the four Taiwanese Indigenous groups relatively equally, auditory exostosis was kept in the present study.

Table 4.6. Summary of the non-metric traits recorded.

Trait	Expression	Original Score	Combined Score
Accessory infraorbital foramen	absent	0	0
	present-single	1	1
	present- multiple	2	
	unobservable	9	9
Accessory mental foramen*	absent	0	0
	present-single	1	1
	present- multiple	2	
	unobservable	9	9
Asterionic bone	absent	0	0
	present	1	1
	unobservable	9	9
Auditory exostosis	absent	0	0
	partial- <1/3	1	1
	partial- >1/3	2	
	unobservable	9	9
Biasterionic suture	absent	0	0
	present	1	1
	unobservable	9	9
Condylus tertius**	absent	0	0
	present	1	1
	unobservable	9	9
Condylar canal patent	not patent	0	0
	patent	1	1
	unobservable	9	9

Table 4.6. Summary of the non-metric traits recorded.

Trait	Expression	Original Score	Combined Score
Hypoglossal canal bridging	absent	0	0
	partial	1	
	complete	2	1
	unobservable	9	9
Jugular foramen bridging**	absent	0	0
	partial	1	
	complete	2	1
	unobservable	9	9
Medial palatine canal	absent	0	0
	partial	1	1
	complete	2	
	unobservable	9	9
Metopism	absent	0	0
	partial	1	1
	complete	2	
	unobservable	9	9
Mylohyoid bridging*	absent	0	0
	partial	1	1
	complete	2	
	unobservable	9	9
Ossicle at lambda	absent	0	0
	present	1	1
	unobservable	9	9
Occipitomastoid bone	absent	0	0
	present	1	1
	unobservable	9	9
Ovale-spinosum confluence	absent	0	0
	partial	1	1
	complete	2	
	unobservable	9	9
Parietal notch bone	absent	0	0
	present	1	1
	unobservable	9	9

Table 4.6. Summary of the non-metric traits recorded.

Trait	Expression	Original Score	Combined Score
Precondylar tubercle**	absent	0	0
	present	1	1
	unobservable	9	9
Supraorbital foramen	absent	0	0
	present- single	1	1
	present- multiple	2	
	unobservable	9	9
Transverse zygomatic suture	absent	0	0
	partial (< 2mm)	1	
	complete	2	1
	unobservable	9	9
Tympanic dehiscence	absent	0	0
	aperture	1	1
	large defect present	2	
	unobservable	9	9
* removed due to lack of sample **removed due to no present in all samples			

The scoring system for each trait is shown in Table 4.6, following the procedures of Hanihara and Ishida (2001a, b, c, d) and Hanihara *et al.* (2003). This scoring system was summarized from the work of Dodo (1974), Hauser and De Stefano (1989) and Ossenberg (1970) and has been used in multiple studies (e.g. Godde 2010, 2013; Movsesian 2013), including the comparative data from Fukumine *et al.* (2006). As mentioned in Chapter 3, the bilateral traits require special attention when recording. Since multiple studies suggested the underlying genes that control each side would more likely be the same (Cesnys 1982; Korey 1980; McGrath *et al.* 1984; Perizonius 1979), counting two sides separately should not be considered. Similarly, if only one particular side of the cranium is used, the information may have been oversimplified, and the

amount of phenotypic information may be reduced (Movsesian 2013). Therefore, two common methods were suggested. The first method by Konigsberg (1990) and Konigsberg *et al.* (1993) suggested that for those bilateral traits, random sides should be selected for scoring to avoid bias. However, in the present study, the individual count method was used in order to be consistent with Fukumine *et al.* (2006). The individual count method suggests that if a trait is present on either or both sides, it should be considered present (Hanihara *et al.* 2003).

Analysis of Error

Craniometric Data

Intra-observer error was tested by re-measuring 20% of the sample using MicroScribe™ G2 digitizing system with the 3Skull program (Ousley 2014). Intraclass correlation coefficients (ICC) for all 40 measurements were used to compare the two trials. The intraclass correlation coefficients were calculated by SPSS 23.0 (IBM Corp. 2015). All measurements showed no statistical differences (95% confidence interval) (Table 4.7). Therefore, no measurements were removed because of intra-observer error.

Table 4.7. ICC of the 40 measurements.

Measurement	ICC	Measurement	ICC	Measurement	ICC
GOL	0.997	MDH	0.979	GLS	0.917
NOL	0.997	OBH	0.975	STB	0.953
BNL	0.995	OBB	0.961	FRC	0.989
BBH	0.998	DKB	0.963	PAC	0.979
XCB	0.991	NDS	0.987	NAR	0.981
XFB	0.983	WNB	0.987	SSR	0.993

Table 4.7. ICC of the 40 measurements.

Measurement	ICC	Measurement	ICC	Measurement	ICC
ZYB	0.988	ZMB	0.975	PRR	0.996
AUB	0.997	FMB	0.991	DKR	0.971
ASB	0.985	NAS	0.980	ZOR	0.979
BPL	0.996	EKB	0.996	FMR	0.977
NPH	0.981	DKS	0.959	EKR	0.983
NLH	0.978	IML	0.951	ZMR	0.934
JUB	0.988	XML	0.984		
NLB	0.975	WMH	0.979		

Inter-observer error was not analyzed in the present study due to the high cost associated with using the collection and lack of other researchers. However, special attention was paid to mastoid height (MDH) due to high rate of discrepancy; Howells (1973) allows 4 mm of discrepancy. As in previous research about measuring error, Ross and Williams (2008) pointed out that *Type III* landmarks showed greater differences in digitizing between observers compared to *Type I* and *Type II* landmarks. These types of landmarks were defined by Bookstein (1997). *Type I* are defined at the juxtaposition of tissue (e.g., lambda), *Type II* are defined at the points of maximum curvature (e.g., basion), and *Type III* are extreme points (e.g. euryon). On the other hand, Sholts *et al.* (2011) pointed out that measurements using 3D digitizers are significantly more precise than the standard measurements, with an overall mean standard deviation of 0.79 mm.

Non-metric Data

Intra-observer error was tested by re-examining the samples from the Pazeh sample, following Molto (1979). The Pearson phi coefficient (φ) was calculated as:

$$\varphi = \frac{P_{11}P_{22} - P_{12}P_{21}}{\sqrt{(P_{1\cdot})(P_{\cdot 1})(P_{2\cdot})(P_{\cdot 2})}}$$

where P_{11} is the number of common absences recorded in both analyses, P_{22} is the number of common presences recorded in both analyses, P_{12} is the number present in the first analysis but absent in the second analysis, P_{21} is the number present in the second analysis but absent in the first analysis, $P_{1\cdot}$ is P_{11} plus P_{12}, $P_{2\cdot}$ is P_{21} plus P_{22}, $P_{\cdot 1}$ is P_{11} plus P_{21}, and $P_{\cdot 2}$ is P_{12} plus P_{22}. The results of the calculation are shown in Table 4.8. It is noted that all traits showed a squared φ coefficient value greater than 0.7, which Molto (1979) suggested as a threshold for observational repeatability. In other words, no traits need to be removed due to intra-observation error. As noted by Molto (1979), all 15 traits used in the present study also showed a low intra-observer error.

Table 4.8. The φ coefficient testing for intra-observer error of the 15 non-metric traits.

Trait	P_{11}	P_{22}	P_{12}	P_{21}	φ	φ^2
Accessory infraorbital foramen	17	16	0	0	1	1
Asterionic bone	28	5	0	0	1	1
Auditory exostosis	30	2	0	0	1	1
Biasterionic suture	32	1	0	0	1	1
Condylar canal patent	13	15	0	1	0.933	0.870

Table 4.8. The φ coefficient testing for intra-observer error of the 15 non-metric traits.

Trait	P_{11}	P_{22}	P_{12}	P_{21}	φ	$φ^2$
Hypoglossal canal bridging	28	4	0	0	1	1
Medial palatine canal	11	21	0	1	0.935	0.874
Metopism	27	4	0	0	1	1
Ossicle at lambda	23	8	0	0	1	1
Occipitomastoid bone	27	5	0	0	1	1
Ovale-spinosum confluence	29	4	0	0	1	1
Parietal notch bone	26	7	0	0	1	1
Supraorbital foramen	18	15	0	0	1	1
Transverse zygomatic suture	27	4	1	0	0.878	0.771
Tympanic dehiscence	26	7	0	0	1	1

Non-metric inter-observer error was not analyzed in this study due to the high cost of the collection and lack of other researchers. However, Ishida and Dodo (1990) presented an inter-observer error test for the traits that were used in this study. The Pearson phi coefficient (φ) was used to calculate the replicability of the observation. The results showed that five of the 15 traits (asterionic bone [0.633], biasterionic suture [0.5787], occipitomastoid bone [0.6495], transverse zygomatic suture [0.4041], and tympanic dehiscence [0.5302]) had a relatively lower φ value and should be used with caution.

Analysis of Data

Craniometric Data

As mentioned in Chapter 3, the biological affinity from craniometric data was estimated by discriminant function analysis and Mahalanobis' generalized distance. However, these analyses do not allow for missing data. Therefore, before any further analysis, all missing data were first adjusted. Two methods were used to replace the missing data. For most of the measurements, missing data were replaced using a regressed value. A total of six measurements were replaced using a regressed value (one basion-prosthion length, one nasion-prosthion height, two naso-dacryal subtenses, one subspinale radius, and one prosthion radius). However, for measurements that show symmetric characteristics (e.g., bizygomatic breadth, bijugal breadth, and bimaxillary breadth), coordinate geometric processes were applied when only one side was damaged.

The procedure of the coordinate geometric process to replace the missing data includes creating the equation of the midplane of the cranium, recording the point from the remaining side and doubling the distance between the point and the midplane. It is noted that the midplane of the cranium is defined by nasion, bregma and lambda. Two bizygomatic breadth, two bijugal breadth and three bimaxillary breadth measurements were replaced using this method.

In order to maximize sample size, a combination of both males and females were used in the present study. Many researchers suggested that a removal of the size-based component may provide a better understanding of the pattern of the variation (e.g., Corruccini 1973; Howells 1989). Though multiple studies (e.g., Green 1990;

Pietrusewsky 1994, 1995) showed that there is little effect to the result of interpreting the patterns of cranial variation when removing size-related component for single sex based samples, many scholars (e.g., Relethford 1994, 2009) suggested that the data would need to be standardized within each sex before combining the data. This process is aimed to eliminate the influence of sex-related size variation. Therefore, in the present study, raw measurements were standardized within each sex before combining.

One of the most common methods to cancel the size influence is C-score (e.g., Brace and Hunt 1990; Brace and Tracer 1992; Brace *et al.* 1989; Brace *et al.* 1990; Brace *et al.* 1991; Brace *et al.* 1993; Howells 1986, 1989; Kawakubo *et al.* 2009; Pietrusewsky 1995). For example, Hanihara (1997) used C-score-based Mahalanobis' generalized distances in the study of estimating the craniofacial affinities of circum-Pacific samples.

The method of standardizing raw data into C-score is a two-step procedure. First, individual raw measurements were converted into sex-specific Z-score, which is calculated as (Bruce and Hunt 1990):

$$Z_{ij} = \frac{\left(X_{ij} - \bar{X}_i\right)}{\sigma_i}$$

Where *i* is the number of the measurement, *j* is the number of the individual. Therefore, X_{ij} is the value of the measurement "*i*" for individual "*j*". $\bar{X}_i$ is the overall sex specific average value for measurement "*i*", and σ_i is the overall sex specific standard deviation for the measurement "*i*".

A PENSIZE (*P*) index is then calculated for each individual, which is calculated as (Howells 1989):

$$\mathrm{PENSIZE} = \frac{\sum_{i=1}^{N} Z_{ij}}{N}$$

Where *N* is the total measurements used (in the present study *N*=40).

The C-score of a given measurement (*i*) of an individual (*j*) is then calculated based on its Z-score and the PENSIZE index of the individual, which is (Howells 1989):

$$C_{ij} = Z_{ij} - P$$

It is noted that for each individual (*j*) the sum of the C-scores of the measurements should equal to zero ($\sum_{i=1}^{N} C_{ij} = 0$) (Howells 1989).

Stepwise discriminant function analysis and Mahalanobis' generalized distance were applied to the C-scores of the 40 measurements for seven samples using *SPSS 23.0* (IBM Corp. 2015). Instead of considering all variables when creating the discriminant function, the stepwise method considered the response of each variable. In each step of the analysis, the variable that created the most separation was entered into the discriminant function ahead of the others. In other words, measurements that aid in differentiating the groups were identified. Furthermore, the stepwise method helps to reduce the influence of high correlation variables.

The number of the discriminant functions that were created is one less than the number of groups that need to be differentiated. The discriminant functions are linear combinations of variables that separate the groups best. In other words:

$$D = a + b_1X_1 + b_2X_2 + \cdots + b_nX_n$$

where D is the discriminant score, x_i is the discriminant variable and b_i is the discriminant coefficient of each discriminant variable (i.e., weight) (Rencher 2002). The eigenvalue of

each discriminant function will also be calculated during the process. In general, discriminant functions with larger eigenvalues suggest a higher power in differentiating the groups, which also means that the functions with small eigenvalues can be ignored. The standardized coefficients may further be calculated. The standardized coefficients reflect the contribution of the variables to the separation of the groups, i.e., the higher the absolute value of the coefficient, the more important the variable is in the given discriminant function. Another important value is the partial F value, which similar to the standardized coefficients, shows the significance of each variable.

Mahalanobis' generalized distance was calculated by following the formula:

$$D^2 = (X - Y)'S^{-1}(X - Y)$$

where X and Y is the matrix of the group centroid, and S is the covariant matrix (Mahalanobis 1936; Rencher 2002). The covariance matrix and group centroid matrixes were calculated by *SPSS 23.0* (IBM Corp. 2015), and the calculation of Mahalanobis' generalized distance was done using Microsoft Excel 2013 (Microsoft Corp. 2012).

Non-metric Data

The biological affinity from non-metric traits data was estimated by calculating the MMD between two populations. Since previous works (e.g., Berry and Berry 1967; Hanihara and Ishida 2001a, b, c, d) suggest that there are minor or no sex differences in frequency, the individuals were not sexed. The frequency of presence for each trait in each population was first calculated. It is noted that multiple scholars (e.g., Green and Suchey 1976; Harris and Sjøvold 2004) have suggested that in order to correct extreme

cases, some adjustment would be required when calculating the frequency. Bartlett (1936) suggests that when the trait does not occur in a population (p=0), its frequency should be adjusted as p=1/4n. Likewise, when the trait always occurs (p=1), it should be adjusted as p=1-(1/4n).

The calculation of MMD was explained in detail by de Souza and Houghton (1977). They pointed out that multiple studies misunderstood the correct formula, which should be:

$$\mathrm{MMD} = \frac{\sum_{k=1}^{r}(\theta_{ik} - \theta_{jk})^2 - \left(\frac{1}{n_{ik}} + \frac{1}{n_{jk}}\right)}{r}$$

where r is the number of traits used in the equation, n_{ik} and n_{jk} is the sample size of group i and j of trait k, and θ_{ik} and θ_{jk} is the $\sin^{-1}$ transformation of the frequency of trait k of group i and j. However, several studies suggest that the formula may overestimate the true variance (Green and Suchey 1976; Green *et al.* 1979; Harris and Sjøvold 2004). Therefore, a better formula, which was corrected by Freeman and Tukey (1950) should be:

$$\mathrm{MMD} = \frac{\sum_{k=1}^{r}(\theta_{ik} - \theta_{jk})^2 - \left(\frac{1}{n_{ik} + \frac{1}{2}} + \frac{1}{n_{jk} + \frac{1}{2}}\right)}{r}$$

and the value of θ is calculated in:

$$\theta = \frac{1}{2}\sin^{-1}\left(1 - \frac{2m}{n+1}\right) + \frac{1}{2}\sin^{-1}\left(1 - 2\left(\frac{m+1}{n+1}\right)\right)$$

where m is the number of occurrences of the trait in the sample and n is the number of the sample; therefore, the frequency of the trait(p) is m/n. However, Harris and Sjøvold

(2004) suggested that a better transformation was created using Anscombe (1948) instead of Freeman and Tukey's transformation for calculating the θ. Though many other researchers also recommended Anscombe's transformation for various reasons (Green and Suchey 1976; Nikita 2015), one of the greatest benefits of this process is that the transformation can be easily written in the form of p, the trait frequency (Harris and Sjøvold 2004). Therefore, this allows an easier comparison to other data sets. The Anscombe's transformation is:

$$\theta = \sin^{-1}\left(1 - 2\left(\frac{m + \frac{3}{8}}{n + \frac{3}{4}}\right)\right)$$

or in the form of trait frequency (p):

$$\theta = \sin^{-1}\left(\left(\frac{1}{1 + \frac{3}{4n}}\right)(1 - 2p)\right)$$

It is noted that there are some mistakes in the formula given in Harris and Sjøvold (2004), which is corrected in this present study.

The standard deviation of the MMD is further calculated in order to check the statistical significance between the two groups. The formula is:

$$\sqrt{\frac{2}{r^2}\sum_{k=1}^{r}\left(\frac{1}{n_{ik}} + \frac{1}{n_{jk}}\right)^2}$$

where *r* is the number of traits used in the equation, n_{ik} and n_{jk} is the sample size of group *i* and *j* of trait *k*. The analysis was done in *SPSS 23.0* (IBM Corp. 2015).

Dendrogram Construction

The Unweighted Pair Group Method with Arithmetic Mean (UPGMA) method (Sokal and Michener 1958) was applied to Mahalanobis' generalized distance and MMD results to construct dendrograms of the relationships. In each step of the clustering process, the nearest two clusters were combined to create a higher level of cluster.

CHAPTER 5: RESULTS

Craniometric Data

The means and standard deviations for 40 raw measurements of the seven samples are presented in Tables 5.1-5.3. Before running the discriminant function analysis, a test of equality of group means of the C-score data was first undertaken using stepwise analysis based on the Wilks' Lambda. This procedure determines how important each variable is in differentiating the cranial series. A variable that shows a statistically significant difference between the samples results in a higher F value (or lower Wilks' Lambda). The results are presented in Tables 5.4 and 5.5 ranked from the highest F value to the lowest F value. Basion-bregma height (BBH), bimaxillary breadth (ZMB), and bijugal breadth (JUB) are the three most important measurements in separating the four Taiwanese Indigenous groups (Table 5.4). Dacryon radius (DKR), naso-dacryal subtense (NDS), and nasion radius (NAR) are the three most important measurements in separating the seven groups (Table 5.5).

In each step of the stepwise analysis, the variable with the smallest Wilks' Lambda was entered into the discriminant function and its contribution to the discriminant function was calculated. Variables with little contribution to the discriminant function were removed from the final discriminant functions. The results show that a total of 9 c-scores representing 9 measurements remained in the final discriminant functions separating the four Taiwanese Indigenous groups, and a total of 17 c-scores representing 17 measurements remained in the final discriminant functions separating the seven groups. Table 5.6 presents the remaining c-scores and their

canonical discriminant function coefficients for three discriminant functions that separate the four Taiwanese Indigenous groups. Table 5.7 presents the remaining c-scores and their canonical discriminant function coefficients for six discriminant functions that separate the seven groups.

Eigenvalues, which indicate the power of the discriminant function in differentiating the groups, are presented in Tables 5.8 and 5.9. The % of variance indicates the percentage of variance accounted for by each function. For example, in the analysis of the four Taiwanese Indigenous groups, the first function accounts for 68.4% the total variation, with a canonical correlation of 0.826, which suggests that the model explains 68.2% (square of the canonical correlation) of the variation in the grouping variable. On the other hand, in the analysis of the seven groups, the first function accounts for 68.4% of the total variation, with a canonical correlation of 0.877, which suggests the model explains 76.9% (square of the canonical correlation) of the variation in the grouping variable. Tables 5.10 and 5.11 (Wilks' Lambda) indicate the percentage of total variability not explained. For example, in the tests of Functions 1 through 3 for the four Taiwanese Indigenous groups analysis, 14.6% of the variation in the grouping variables was unexplained. It also indicates that the functions were statistically significant ($p<0.000$). As for the analysis of the seven groups, in tests of Functions 1 through 6, 6.4% of the variation in the grouping variables were unexplained. It also indicates that the functions were statistically significant ($p<0.000$).

Table 5.12 shows the discriminant scores of the centroid of each group in each discriminant function in the analysis of the Taiwanese Indigenous groups. The first two

discriminant functions, which account for 91.9% of the total variation (Table 5.8), were used to create a scatter plot (Figure 5.1). The scatter plot shows that the groups were well separated from each other.

Table 5.13 shows the discriminant scores of the centroid of each group in each discriminant function in the analysis of the seven groups. The first two discriminant functions, which account for 82.7% of the total variation (Table 5.9), were used to create a scatter plot (Figure 5.2). The scatter plot shows that the groups were well separated from each other, with three general clusters present.

A cross-validation was also produced in order to check the power of the discriminant functions. The results (Tables 5.14 and 5.15) indicate the percentage of correctly classified cases and the percentage of misclassified cases. A total of 70.3% of cross-validation grouped cases were correctly classified in the analysis of the Taiwanese Indigenous group, and a total of 63% of cross-validation grouped cases were correctly classified in the analysis of the seven groups. The correction rate of each group is relatively high in both analyses, except for the Pazeh group, which was often misclassified as Babuza.

Mahalanobis' generalized distances using 9 c-scores representing 9 measurements in separating the four Taiwanese Indigenous groups are presented in Table 5.16. The mountain indigenous groups generally showed smaller distance with each other, as did the lowland indigenous. The dendrogram based on the calculated Mahalanobis' generalized distances is presented in Figure 5.3. Two distinct clusters are evident in the dendrogram (the results of each step of the UPGMA process are given in Appendix A).

Mahalanobis' generalized distances using 17 c-scores representing 17 measurements in separating the seven groups are presented in Table 5.17. The Taiwanese Indigenous groups generally showed smaller distances from each other. The comparative groups (South Japan, Hainan, and Philippines) also showed small distances from each other. The dendrogram based on the calculated Mahalanobis' generalized distances is presented in Figure 5.4. Three distinct clusters are evident in the dendrogram (the results of each step of the UPGMA process are given in Appendix A).

Table 5.1. Means and standard deviations for 40 raw measurements for seven cranial samples (combined sex).

	Atayal (n=34)		Babuza (n=30)		Bunun (n=24)		Pazeh (n=23)		S Japan (n=91)		Hainan (n=83)		Philippines (n=50)	
Measurement	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**
GOL	172.6	6.6	178.3	6.8	180.8	8.7	175.6	7.4	177.3	7.1	173.7	6.6	176.9	6.9
NOL	169.4	6.3	176.4	6.5	178.4	8.1	173.1	6.7	175.6	6.7	172.1	6.1	174.8	6.7
BNL	96.1	3.7	98.5	4.4	100.0	4.2	99.4	4.5	99.1	4.8	97.3	4.4	98.5	3.9
BBH	129.9	5.0	137.8	5.6	130.4	5.0	136.3	5.1	135.0	5.6	134.6	4.7	134.8	5.1
XCB	133.6	5.5	141.4	5.0	137.9	5.3	137.1	6.3	136.2	4.9	136.9	4.8	139.8	5.6
XFB	109.6	5.3	113.5	4.8	111.8	4.9	111.0	6.9	113.1	4.7	113.4	5.2	115.2	4.7
ZYB	128.1	6.6	132.8	6.5	129.8	6.0	131.2	5.5	129.6	6.0	130.1	6.3	133.2	5.8
AUB	118.9	5.9	124.4	5.5	121.8	4.8	121.2	5.2	120.4	5.0	120.8	5.1	123.0	5.3
ASB	107.1	5.2	108.4	5.7	107.3	4.8	105.1	4.3	106.1	4.7	104.0	4.3	107.3	4.5
BPL	92.6	5.0	94.7	4.5	96.0	4.5	95.4	5.4	97.2	5.1	95.1	5.5	97.9	4.7
NPH	62.8	4.6	68.3	4.6	67.2	4.6	67.0	4.5	67.6	4.0	67.7	4.4	66.8	3.3
NLH	48.4	3.0	52.1	3.2	52.1	3.5	51.1	2.6	50.7	2.9	51.0	3.0	51.5	2.2
JUB	110.5	5.9	117.2	5.8	112.3	4.6	115.2	5.3	114.4	5.5	115.9	5.4	118.2	4.6
NLB	25.8	2.1	25.7	2.1	25.9	1.7	26.9	2.1	25.8	1.7	26.7	2.1	28.3	1.6
MDH	25.4	2.7	27.8	3.6	26.1	3.5	26.7	4.2	27.9	3.7	29.6	2.9	27.5	3.3
OBH	33.5	1.7	34.3	2.3	34.9	2.2	34.0	1.9	34.0	1.6	33.3	2.0	33.2	1.5
OBB	37.4	2.0	38.7	1.7	37.8	1.4	38.3	2.0	38.6	1.7	38.2	1.7	39.0	1.4
DKB	20.6	2.4	20.8	2.0	21.9	2.5	22.2	3.2	21.1	1.9	21.6	1.9	22.6	1.7
NDS	9.0	1.7	8.5	1.5	9.6	2.4	8.6	1.7	7.6	1.2	8.2	1.3	8.5	1.3
WNB	8.0	2.0	8.2	2.2	8.2	1.4	8.4	2.5	6.9	1.7	7.8	2.0	8.1	2.2
ZMB	91.9	5.7	100.6	5.5	96.1	3.6	98.7	5.9	95.3	5.3	96.9	4.2	98.2	4.3
FMB	94.6	4.5	96.3	4.6	96.9	4.5	97.3	4.5	94.5	4.2	95.2	3.8	98.1	3.3

Table 5.1. (continued) Means and standard deviations for 40 raw measurements for seven cranial samples (combined sex).

	Atayal (n=34)		Babuza (n=30)		Bunun (n=24)		Pazeh (n=23)		S Japan (n=91)		Hainan (n=83)		Philippines (n=50)	
Measurement	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**
NAS	13.6	2.2	12.8	2.0	14.8	2.3	15.0	2.6	14.7	2.0	14.9	2.2	15.6	2.1
EKB	92.9	4.4	96.1	3.5	94.8	3.7	96.2	4.4	95.8	3.8	96.1	3.6	98.4	3.3
DKS	9.7	1.8	9.2	2.2	10.0	2.1	9.9	2.2	9.2	1.7	9.0	1.9	9.1	1.7
IML	33.5	3.2	36.0	3.5	33.0	2.8	33.4	3.9	33.4	3.4	34.8	3.3	36.1	3.4
XML	50.1	3.2	55.0	4.0	51.4	3.9	52.0	4.4	51.5	4.1	53.1	3.5	52.8	3.7
WMH	20.1	2.2	25.2	2.8	22.8	2.8	23.7	2.7	22.8	2.8	24.7	2.0	23.0	2.3
GLS	1.8	0.9	1.8	0.8	2.5	1.0	2.1	0.9	2.3	1.1	2.6	0.9	3.5	1.0
STB	107.6	5.8	111.3	5.3	109.3	6.6	109.5	7.1	110.2	5.7	110.5	5.8	112.4	5.8
FRC	105.7	5.5	111.9	5.5	109.2	5.2	110.9	5.4	108.9	5.0	108.9	4.2	110.9	4.6
PAC	111.4	6.2	114.1	5.1	112.5	5.1	111.0	7.1	111.9	5.8	110.6	5.7	111.6	6.6
NAR	86.4	3.2	88.6	4.3	91.5	4.7	88.4	4.2	91.6	4.6	90.3	3.7	92.2	3.7
SSR	86.2	4.1	90.3	4.5	92.8	4.8	90.9	4.7	92.7	4.9	91.3	4.3	94.1	3.8
PRR	93.1	5.5	96.7	5.1	98.7	4.8	97.3	6.3	99.9	5.0	98.5	4.9	101.9	4.4
DKR	75.7	3.5	78.7	3.4	79.8	4.4	78.3	3.5	82.1	4.2	80.5	3.3	81.6	3.4
ZOR	73.8	3.7	77.0	3.4	78.1	4.3	76.8	4.1	79.6	4.3	78.5	3.2	79.5	3.7
FMR	73.0	3.7	75.8	3.5	76.7	4.1	74.4	3.3	77.5	4.1	76.1	3.3	77.2	3.3
EKR	66.9	3.5	69.9	3.9	70.3	3.3	69.3	3.3	72.8	4.1	71.2	3.0	72.0	3.3
ZMR	66.2	3.6	69.8	4.1	69.7	4.1	68.8	4.3	71.3	4.2	70.3	3.5	72.3	3.8

Table 5.2. Means and standard deviations for 40 raw measurements for seven cranial samples (male).

	Atayal (n=21)		Babuza (n=18)		Bunun (n=17)		Pazeh (n=14)		S Japan (n=50)		Hainan (n=45)		Philippines (n=50)	
Measurement	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**
GOL	174.9	7.2	185.2	5.8	180.3	5.9	178.0	5.3	181.3	5.7	176.4	6.1	176.9	6.9
NOL	171.2	7.2	182.6	5.3	178.2	5.6	175.5	4.5	179.2	5.3	174.4	5.9	174.8	6.7
BNL	97.0	4.0	101.7	3.4	100.5	3.9	100.9	4.4	101.9	3.7	99.5	4.0	98.5	3.9
BBH	131.0	5.1	132.2	4.5	140.8	4.4	137.8	5.2	138.3	4.1	136.7	4.5	134.8	5.1
XCB	134.5	3.8	139.1	5.6	143.3	3.8	138.2	5.5	138.3	4.6	138.4	4.3	139.8	5.6
XFB	110.6	4.0	113.5	4.0	115.4	3.4	113.1	6.5	115.1	3.9	114.7	4.9	115.2	4.7
ZYB	130.4	6.7	133.1	2.6	136.0	5.2	133.6	4.7	133.6	3.9	134.0	4.6	133.2	5.8
AUB	120.5	5.7	124.0	3.3	126.6	5.0	123.0	4.8	122.9	4.2	123.6	3.8	123.0	5.3
ASB	108.5	4.2	108.6	3.9	109.4	6.4	105.2	4.3	108.1	3.8	106.0	3.9	107.3	4.5
BPL	93.5	5.3	96.4	4.6	96.5	4.2	97.4	4.4	99.3	4.6	96.6	5.7	97.9	4.7
NPH	63.9	5.0	68.9	4.0	70.6	3.2	68.9	3.9	69.0	3.7	69.7	3.8	66.8	3.3
NLH	49.0	3.3	53.9	2.3	53.7	2.3	52.0	2.7	51.8	2.7	52.4	2.5	51.5	2.2
JUB	112.4	6.2	114.4	2.9	119.8	4.3	117.3	3.9	117.5	4.5	118.9	4.3	118.2	4.6
NLB	26.4	2.2	26.3	1.6	25.8	1.7	27.1	1.6	26.1	1.7	27.3	1.9	28.3	1.6
MDH	26.4	2.8	27.5	2.9	29.5	3.0	28.5	2.3	30.1	3.8	29.5	2.5	29.6	2.9
OBH	33.8	1.9	35.7	1.6	34.7	2.2	34.4	1.9	34.0	1.6	33.6	2.1	33.2	1.5
OBB	37.8	1.9	38.2	1.2	39.2	1.7	38.7	1.5	39.3	1.6	38.7	1.6	39.0	1.4
DKB	20.5	2.1	22.5	2.6	20.7	2.3	22.8	3.1	21.5	2.1	22.2	1.7	22.6	1.7
NDS	9.2	1.9	10.2	2.4	8.8	1.5	8.7	1.7	7.9	1.2	8.4	1.3	8.5	1.3
WNB	7.8	1.6	8.1	1.2	7.9	2.1	8.3	1.8	6.7	1.8	8.1	2.1	8.1	2.2
ZMB	93.8	5.9	97.4	2.7	102.0	5.8	101.3	4.1	98.0	4.6	98.2	4.0	98.2	4.3
FMB	95.7	4.2	98.8	3.1	98.5	3.7	98.6	4.3	96.9	3.7	97.1	3.0	98.1	3.3

Table 5.2. (continued) Means and standard deviations for 40 raw measurements for seven cranial samples (male).

	Atayal (n=21)		Babuza (n=18)		Bunun (n=17)		Pazeh (n=14)		S Japan (n=50)		Hainan (n=45)		Philippines (n=50)	
Measurement	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**
NAS	13.4	2.5	15.4	1.9	13.1	2.1	15.5	3.0	15.4	1.8	15.4	2.1	15.6	2.1
EKB	94.3	4.5	96.0	3.4	97.2	3.1	97.7	3.5	97.5	3.7	97.9	3.0	98.4	3.3
DKS	9.7	1.9	10.3	2.2	8.9	2.4	10.4	1.9	9.5	1.6	9.2	1.8	9.1	1.7
IML	33.7	3.2	33.8	2.6	37.6	3.3	34.1	3.6	34.5	3.2	35.8	3.1	36.1	3.4
XML	50.9	3.3	52.4	4.0	57.2	3.1	53.5	3.0	53.7	3.5	54.7	3.1	52.8	3.7
WMH	20.5	2.4	23.4	2.8	26.2	2.6	24.7	1.5	23.5	2.8	24.9	1.9	23.0	2.3
GLS	2.2	0.8	2.8	1.0	2.2	0.7	2.2	0.9	2.8	1.1	3.0	0.8	3.5	1.0
STB	108.6	4.2	110.0	7.1	113.2	4.5	110.9	7.2	112.2	5.0	110.9	6.3	112.4	5.8
FRC	107.7	5.0	111.9	3.2	114.4	4.4	112.5	5.2	111.0	4.3	109.4	4.3	110.9	4.6
PAC	112.3	6.6	114.4	4.6	115.6	3.8	112.3	6.5	113.8	5.9	112.0	5.0	111.6	6.6
NAR	87.6	3.4	93.4	3.9	90.0	4.4	89.9	3.4	94.1	3.5	92.2	3.3	92.2	3.7
SSR	87.0	4.3	94.1	4.9	92.1	4.5	93.1	3.3	95.1	4.3	93.0	4.3	94.1	3.8
PRR	94.4	5.6	99.5	4.9	98.8	4.8	99.7	4.6	102.0	4.6	100.2	5.0	101.9	4.4
DKR	76.8	3.6	80.6	4.8	79.8	3.6	79.6	2.9	84.2	3.3	81.9	3.1	81.6	3.4
ZOR	75.0	3.2	78.7	4.8	78.4	3.4	78.0	3.0	81.4	3.8	79.6	3.2	79.5	3.7
FMR	74.7	3.2	77.7	4.1	76.8	3.9	75.6	2.6	79.1	3.5	77.1	2.8	77.2	3.3
EKR	68.3	3.1	71.0	3.6	71.4	4.1	70.0	2.6	74.6	3.7	72.1	2.9	72.0	3.3
ZMR	67.3	3.7	70.4	4.4	71.7	3.5	70.1	3.1	72.9	3.7	71.4	3.1	72.3	3.8

Table 5.3. Means and standard deviations for 40 raw measurements for seven cranial samples (female).

	Atayal (n=13)		Babuza (n=12)		Bunun (n=7)		Pazeh (n=9)		S Japan (n=41)		Hainan (n=38)		Philippines (n=0)	
Measurement	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**
GOL	169.1	3.3	170.0	3.2	175.2	7.2	171.9	9.0	172.5	5.5	170.6	5.7	-	-
NOL	166.5	3.1	168.3	2.8	173.8	7.1	169.3	8.1	171.2	5.6	169.4	5.2	-	-
BNL	94.6	2.7	96.0	3.4	95.5	3.4	97.0	3.7	95.6	3.5	94.7	3.4	-	-
BBH	128.1	4.5	126.0	3.0	133.4	4.0	134.1	4.4	130.9	4.2	132.1	3.7	-	-
XCB	132.2	7.4	134.9	3.4	138.5	5.3	135.3	7.3	133.7	4.1	135.0	4.8	-	-
XFB	108.2	6.9	107.6	4.4	110.6	5.2	107.8	6.6	110.6	4.4	111.8	5.1	-	-
ZYB	124.4	4.6	121.6	3.2	128.1	5.5	127.6	4.6	124.8	4.4	125.6	4.7	-	-
AUB	116.2	5.5	116.3	3.4	121.1	4.5	118.3	4.8	117.3	4.2	117.4	4.4	-	-
ASB	104.8	5.9	104.0	5.5	107.0	4.3	105.0	4.4	103.7	4.5	101.6	3.5	-	-
BPL	91.2	4.3	95.1	4.2	92.1	3.7	92.4	5.7	94.6	4.3	93.4	4.7	-	-
NPH	61.1	3.3	62.9	2.4	64.8	4.1	64.0	3.8	65.9	3.7	65.4	3.9	-	-
NLH	47.5	2.3	47.7	1.4	49.6	2.8	49.8	1.9	49.4	2.5	49.3	2.8	-	-
JUB	107.4	3.9	107.3	4.1	113.3	5.6	111.9	5.7	110.7	4.1	112.4	4.3	-	-
NLB	24.7	1.4	24.9	1.5	25.5	2.6	26.6	2.8	25.4	1.7	26.0	2.1	-	-
MDH	23.8	1.7	22.7	2.5	25.3	3.0	23.8	5.1	25.2	2.7	25.2	2.9	-	-
OBH	33.0	1.5	32.9	2.0	33.8	2.4	33.3	1.9	33.9	1.5	32.8	1.8	-	-
OBB	36.6	2.0	36.9	1.5	38.0	1.5	37.7	2.5	37.7	1.4	37.6	1.5	-	-
DKB	20.6	2.9	20.4	1.3	20.9	1.5	21.3	3.2	20.7	1.6	20.9	2.1	-	-
NDS	8.7	1.2	8.0	1.7	8.0	1.5	8.3	1.7	7.2	1.0	7.9	1.2	-	-
WNB	8.4	2.4	8.4	2.0	8.8	2.2	8.4	3.5	7.2	1.6	7.5	1.8	-	-
ZMB	88.8	3.7	93.0	3.9	98.6	4.5	94.7	6.2	92.0	4.3	95.3	3.9	-	-
FMB	92.8	4.6	92.3	4.2	92.9	3.7	95.3	4.3	91.7	2.9	92.8	3.4	-	-

Table 5.3. (continued) Means and standard deviations for 40 raw measurements for seven cranial samples (female).

	Atayal (n=13)		Babuza (n=12)		Bunun (n=7)		Pazeh (n=9)		S Japan (n=41)		Hainan (n=38)		Philippines (n=0)	
Measurement	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**
NAS	13.8	1.9	13.1	2.6	12.4	1.9	14.3	1.7	13.9	2.0	14.3	2.1	-	-
EKB	90.7	3.4	92.0	3.2	94.4	3.7	93.8	4.8	93.7	3.0	94.1	3.2	-	-
DKS	9.8	1.8	9.4	1.9	9.6	1.8	9.1	2.4	8.9	1.7	8.8	2.0	-	-
IML	33.1	3.3	31.0	2.4	33.7	2.4	32.3	4.4	32.0	3.0	33.7	3.2	-	-
XML	48.7	2.8	48.9	2.4	51.7	2.8	49.8	5.5	48.9	3.2	51.3	3.0	-	-
WMH	19.5	1.9	21.4	2.1	23.8	2.6	22.0	3.4	22.0	2.6	24.6	2.0	-	-
GLS	1.1	0.6	2.0	1.0	1.2	0.6	1.9	0.9	1.7	0.8	2.2	0.9	-	-
STB	106.0	7.7	107.6	5.4	108.5	5.3	107.3	6.7	107.7	5.5	109.9	5.1	-	-
FRC	102.5	4.8	102.6	1.8	108.3	5.0	108.4	5.0	106.4	4.7	108.3	4.1	-	-
PAC	110.0	5.3	107.9	2.8	111.8	6.1	108.9	7.9	109.6	4.6	109.0	6.2	-	-
NAR	84.6	1.7	87.0	3.2	86.4	3.2	86.2	4.5	88.5	3.8	88.1	2.9	-	-
SSR	85.0	3.7	89.9	3.4	87.6	3.0	87.6	4.7	89.8	3.8	89.2	3.3	-	-
PRR	91.2	4.8	96.7	4.3	93.5	3.9	93.6	7.1	97.4	4.3	96.6	4.1	-	-
DKR	73.9	2.5	77.6	2.4	77.1	2.5	76.3	3.7	79.6	3.8	78.8	2.7	-	-
ZOR	71.8	3.6	76.6	2.2	74.9	2.2	75.0	5.0	77.3	3.8	77.1	2.6	-	-
FMR	70.4	2.9	74.1	3.1	74.3	2.2	72.6	3.7	75.4	3.8	74.8	3.4	-	-
EKR	64.6	2.8	68.7	2.1	67.7	2.2	68.1	4.0	70.5	3.5	70.1	2.7	-	-
ZMR	64.5	2.6	67.9	2.7	67.0	3.3	66.8	5.2	69.4	4.0	69.1	3.6	-	-

Table 5.4. Test of equality of group means in the analysis of the four Taiwanese Indigenous groups (C-scores).

Measurement	Wilks' Lambda	F	df1	df2	Sig.	Measurement	Wilks' Lambda	F	df1	df2	Sig.
BBH	0.623	21.624	3	107	0.000	ZYB	0.914	3.345	3	107	0.022
ZMB	0.746	12.168	3	107	0.000	BNL	0.923	2.972	3	107	0.035
JUB	0.761	11.195	3	107	0.000	AUB	0.928	2.777	3	107	0.045
NAS	0.770	10.683	3	107	0.000	NPH	0.930	2.689	3	107	0.050
WMH	0.794	9.226	3	107	0.000	WNB	0.930	2.666	3	107	0.052
NAR	0.802	8.824	3	107	0.000	PAC	0.931	2.635	3	107	0.054
XML	0.841	6.732	3	107	0.000	DKR	0.941	2.231	3	107	0.089
SSR	0.845	6.533	3	107	0.000	PRR	0.942	2.179	3	107	0.095
NOL	0.847	6.451	3	107	0.000	ZOR	0.943	2.142	3	107	0.099
NDS	0.861	5.736	3	107	0.001	FMR	0.946	2.052	3	107	0.111
IML	0.864	5.620	3	107	0.001	MDH	0.947	1.994	3	107	0.119
NLB	0.865	5.571	3	107	0.001	EKB	0.951	1.819	3	107	0.148
DKS	0.869	5.354	3	107	0.002	FMB	0.962	1.415	3	107	0.243
ASB	0.875	5.109	3	107	0.002	BPL	0.963	1.366	3	107	0.257
GLS	0.880	4.841	3	107	0.003	OBB	0.965	1.275	3	107	0.287
XCB	0.894	4.213	3	107	0.007	OBH	0.968	1.191	3	107	0.317
DKB	0.898	4.065	3	107	0.009	XFB	0.977	0.822	3	107	0.484
GOL	0.904	3.807	3	107	0.012	STB	0.979	0.757	3	107	0.521
FRC	0.910	3.508	3	107	0.018	EKR	0.979	0.750	3	107	0.524
NLH	0.911	3.483	3	107	0.018	ZMR	0.989	0.411	3	107	0.745

df1= degrees of freedom between df2= degree of freedom within.

Table 5.5. Test of equality of group means in the analysis of the seven groups (C-scores).

Measurement	Wilks' Lambda	F	df1	df2	Sig.	Measurement	Wilks' Lambda	F	df1	df2	Sig.
DKR	0.721	21.111	6	328	0.000	FMB	0.893	6.550	6	328	0.000
NDS	0.786	14.851	6	328	0.000	DKS	0.894	6.461	6	328	0.000
NAR	0.787	14.837	6	328	0.000	IML	0.902	5.961	6	328	0.000
EKR	0.807	13.039	6	328	0.000	FMR	0.902	5.928	6	328	0.000
WMH	0.814	12.465	6	328	0.000	OBH	0.904	5.832	6	328	0.000
BBH	0.825	11.630	6	328	0.000	ZMR	0.909	5.505	6	328	0.000
ZOR	0.835	10.804	6	328	0.000	NPH	0.917	4.953	6	328	0.000
NLB	0.839	10.513	6	328	0.000	DKB	0.925	4.435	6	328	0.000
ASB	0.846	9.920	6	328	0.000	XCB	0.929	4.197	6	328	0.000
ZMB	0.850	9.628	6	328	0.000	PAC	0.934	3.839	6	328	0.001
NOL	0.851	9.607	6	328	0.000	AUB	0.935	3.782	6	328	0.001
SSR	0.851	9.551	6	328	0.000	EKB	0.943	3.282	6	328	0.004
JUB	0.852	9.504	6	328	0.000	ZYB	0.947	3.061	6	328	0.006
GOL	0.856	9.174	6	328	0.000	BPL	0.948	2.998	6	328	0.007
WNB	0.865	8.562	6	328	0.000	FRC	0.952	2.760	6	328	0.012
GLS	0.867	8.356	6	328	0.000	NLH	0.953	2.712	6	328	0.014
PRR	0.868	8.312	6	328	0.000	MDH	0.964	2.050	6	328	0.059
BNL	0.875	7.842	6	328	0.000	OBB	0.973	1.519	6	328	0.171
XML	0.877	7.698	6	328	0.000	XFB	0.975	1.397	6	328	0.215
NAS	0.889	6.822	6	328	0.000	STB	0.988	0.648	6	328	0.692

df1= degrees of freedom between df2= degree of freedom within.

Table 5.6. Canonical discriminant function coefficients based on c-scores in the analysis of the four Taiwanese Indigenous groups.

	Function		
Measurement	**1**	**2**	**3**
GOL	-2.506	2.113	-0.088
NOL	2.537	-3.030	0.321
BBH	1.020	0.754	-0.205
XCB	0.426	-0.495	-0.026
ASB	-0.440	0.377	0.497
JUB	0.707	0.365	-0.071
NAS	-0.331	0.355	-0.513
IML	0.204	0.253	0.676
WMH	0.512	-0.090	-0.168
(Constant)	0.343	0.011	-0.353

Table 5.7. Canonical discriminant function coefficients based on c-scores in the analysis of the seven groups.

	Function					
Measurement	**1**	**2**	**3**	**4**	**5**	**6**
BNL	-0.347	-0.002	-0.347	0.278	0.739	-0.151
BBH	0.419	0.816	0.117	0.726	0.021	0.043
XFB	0.580	-0.121	0.157	-0.098	0.362	0.651
NPH	0.394	0.285	-0.256	0.106	0.629	0.160
JUB	0.722	0.419	0.661	0.427	-0.205	0.338
NLB	0.359	-0.064	0.670	0.384	0.081	0.006
MDH	0.453	-0.151	-0.079	0.204	-0.115	0.413
NDS	-0.395	-0.040	0.351	-0.283	0.398	0.803
FMB	-1.406	-0.173	0.368	-0.023	0.527	-0.378
NAS	1.269	-0.315	0.059	0.543	0.288	-0.463
EKB	1.279	0.276	-0.266	0.091	0.361	0.149
DKS	-0.928	0.237	0.018	0.825	0.464	0.691
XML	-0.127	0.439	0.244	-0.078	0.301	0.677
WMH	0.075	0.645	0.364	-0.419	0.659	-0.321
GLS	0.214	-0.308	0.479	-0.163	0.323	0.094
DKR	1.507	-0.108	0.453	-1.737	0.040	0.486
EKR	0.115	-0.161	-0.433	1.811	0.938	0.626
(Constant)	0.000	0.000	0.000	-0.001	-0.001	0.000

Table 5.8. Table of eigenvalues based on c-scores in the analysis of the four Taiwanese Indigenous groups.

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	2.151	68.4	68.4	0.826
2	0.738	23.5	91.9	0.652
3	0.254	8.1	100.0	0.450

First 3 canonical discriminant functions were used in the analysis.

Table 5.9. Table of eigenvalues based on c-scores in the analysis of the seven groups.

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	3.346	68.4	68.4	0.877
2	0.701	14.3	82.7	0.642
3	0.441	9.0	91.7	0.553
4	0.171	3.5	95.2	0.382
5	0.134	2.7	97.9	0.343
6	0.101	2.1	100.0	0.303

First 6 canonical discriminant functions were used in the analysis.

Table 5.10. Table of Wilks' Lambda based on c-scores in the analysis of the four Taiwanese Indigenous groups.

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1 through 3	0.146	199.438	27.000	0.000
2 through 3	0.459	80.638	16.000	0.000
3	0.797	23.443	7.000	0.001

Table 5.11. Table of Wilks' Lambda based on c-scores in the analysis of the seven groups.

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1 through 6	0.064	884.001	102	0.000
2 through 6	0.279	410.892	80	0.000
3 through 6	0.475	239.779	60	0.000
4 through 6	0.684	122.126	42	0.000
5 through 6	0.801	71.334	26	0.000
6	0.908	30.907	12	0.002

Table 5.12. Discriminant scores of the group centroids in the analysis of the four Taiwanese Indigenous groups based on c-scores.

	Function		
Sample	**1**	**2**	**3**
Atayal	-1.326	0.803	0.354
Bunun	-1.271	-1.395	-0.164
Babuza	2.015	-0.256	0.399
Pazeh	0.658	0.602	-0.873

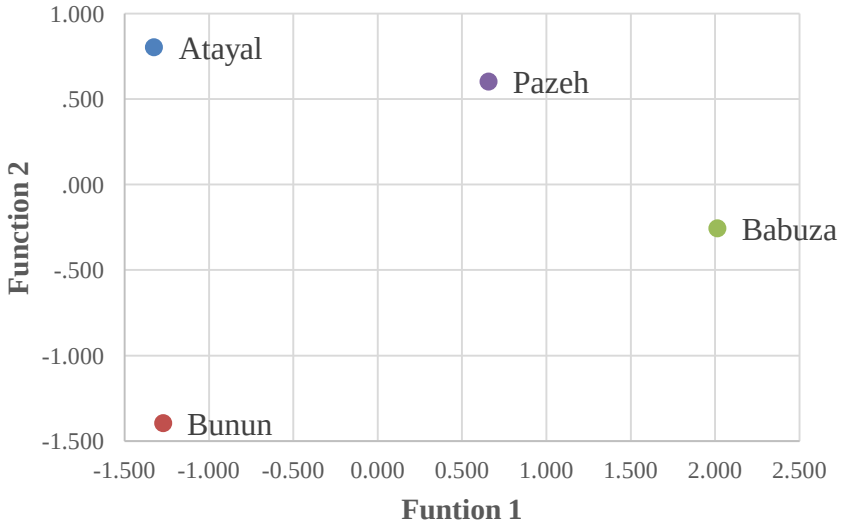

Figure 5.1. Scatter plot of the group centroids on the first two functions in the analysis of Taiwanese Indigenous groups.

Table 5.13. Discriminant scores of the group centroids in the analysis of the seven groups based on c-scores.

	Function					
Sample	**1**	**2**	**3**	**4**	**5**	**6**
Atayal	-3.168	-0.648	0.326	0.516	-0.029	0.574
Babuza	-3.172	-1.114	-0.505	-0.914	0.443	-0.313
Bunun	-1.907	1.893	-0.241	-0.383	-0.607	0.029
Pazeh	-1.592	0.714	0.202	0.879	0.331	-0.800
S. Japan	1.327	-0.216	-0.906	0.152	-0.042	0.049
Hainan	1.279	0.495	0.556	-0.166	0.374	0.151
Philippines	1.016	-0.917	0.799	-0.087	-0.525	-0.229

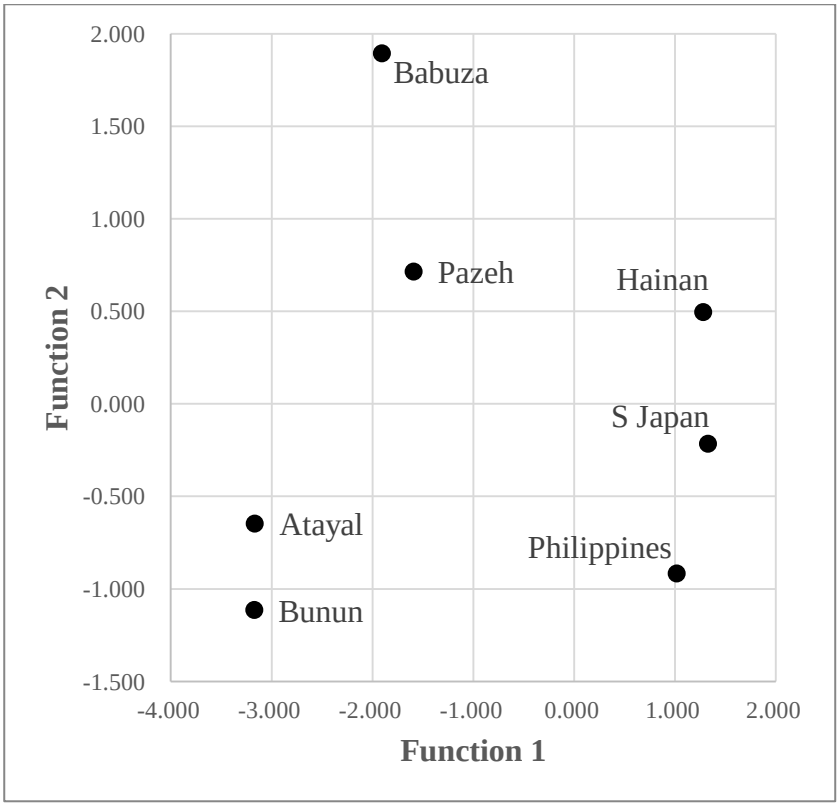

Figure 5.2. Scatter plot of the group centroids on the first two functions in the analysis of seven groups.

Table 5.14. Cross-validation result from stepwise discriminant function analysis of the four Taiwanese Indigenous groups.

		Predicted Group Membership			
	Group	**Atayal**	**Bunun**	**Babuza**	**Pazeh**
Count	**Atayal**	26	4	0	4
	Bunun	2	18	3	1
	Babuza	2	1	24	3
	Pazeh	6	0	7	10
%	**Atayal**	76.5	11.8	0.0	11.8
	Bunun	8.3	75.0	12.5	4.2
	Babuza	6.7	3.3	80.0	10.0
	Pazeh	26.1	0.0	30.4	43.5

Table 5.15. Cross-validation result from stepwise discriminant function analysis of the seven groups.

		Predicted Group Membership						
	Group	**Atayal**	**Bunun**	**Babuza**	**Pazeh**	**S. Japan**	**Hainan**	**Philippines**
Count	**Atayal**	21	6	1	5	0	0	1
	Bunun	9	13	1	0	0	1	0
	Babuza	2	0	22	3	3	0	0
	Pazeh	4	1	8	4	2	2	2
	S Japan	0	0	0	0	66	15	10
	Hainan	0	0	2	1	17	59	4
	Philippines	0	0	0	0	11	13	26
%	**Atayal**	61.8	17.6	2.9	14.7	0.0	0.0	2.9
	Bunun	37.5	54.2	4.2	0.0	0.0	4.2	0.0
	Babuza	6.7	0.0	73.3	10.0	10.0	0.0	0.0
	Pazeh	17.4	4.3	34.8	17.4	8.7	8.7	8.7
	S Japan	0.0	0.0	0.0	0.0	72.5	16.5	11.0
	Hainan	0.0	0.0	2.4	1.2	20.5	71.1	4.8
	Philippines	0.0	0.0	0.0	0.0	22.0	26.0	52.0

Table 5.16. Mahalanobis' generalized distance based on 9 c-scores representing 9 measurements in the analysis of the four Taiwanese Indigenous groups.

Group	Atayal	Bunun	Babuza	Pazeh
Atayal	-	5.915	11.652	7.264
Bunun		-	10.684	8.530
Babuza			-	4.041
Pazeh				-

significant at 1% level.

Table 5.17. Mahalanobis' generalized distance based on 17 c-scores representing 17 measurements in the analysis of the seven groups.

Group	Atayal	Bunun	Babuza	Pazeh	S. Japan	Hainan	Philippines
Atayal	-	5.457	12.685	8.906	23.401	23.879	27.325
Bunun		-	20.548	18.903	32.110	31.843	35.636
Babuza			-	4.435*	23.544	16.173	36.261
Pazeh				-	16.853	10.298	17.994
S. Japan					-	3.489	4.271
Hainan						-	3.857
Philippines							-

* not significant at 1% level.

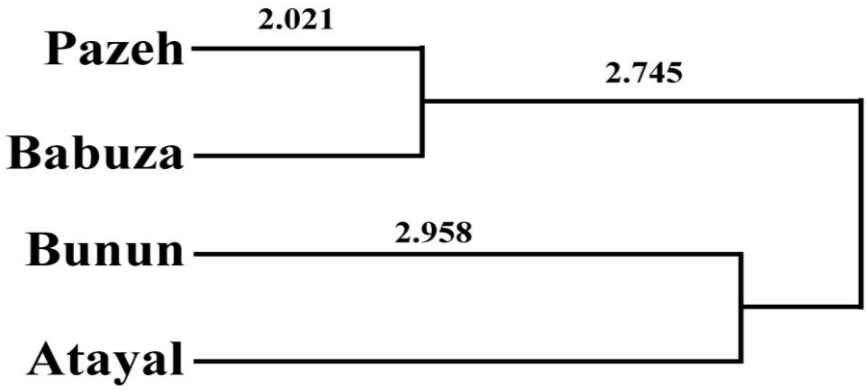

Figure 5.3. Dendrogram of the relationship of the four Taiwanese Indigenous samples based on Mahalanobis' generalized distance using 9 c-scores representing 9 measurements.

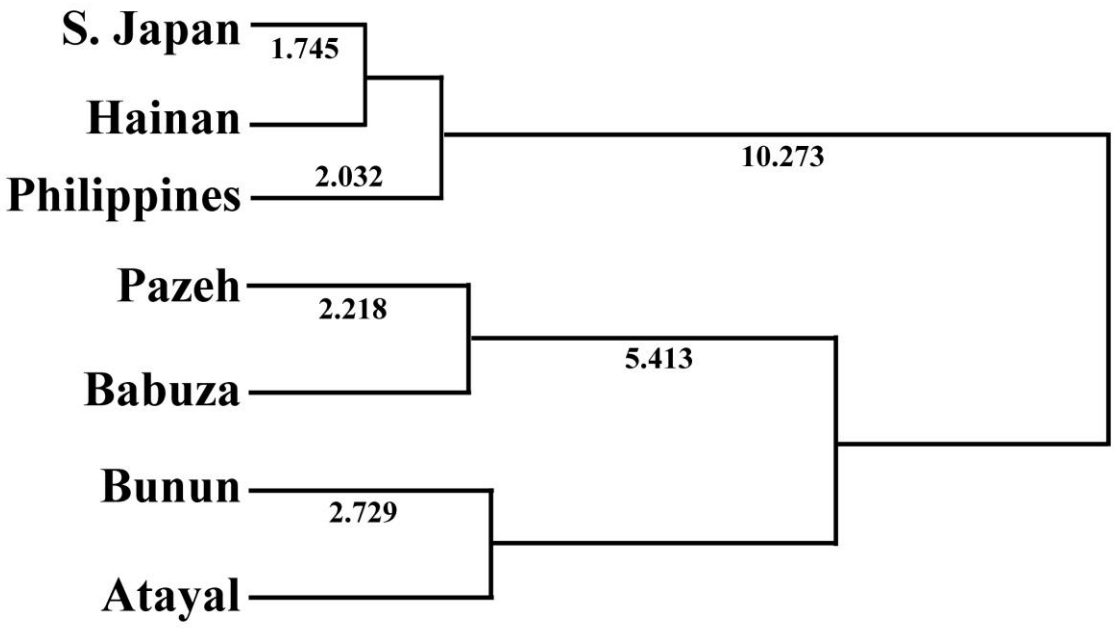

Figure 5.4. Dendrogram of the relationship of the 7 cranial samples based on Mahalanobis' generalized distance using 17 c-scores representing 17 measurements.

Non-metric Data

The frequencies of the non-metric traits for 8 cranial samples are presented in Table 5.18. The frequencies of the traits between each group were highly variable. The medial palatine canal shows a high frequency in Taiwanese Indigenous groups, but the parietal notch bone and tympanic dehiscence showed a relatively low frequency compared to the comparative samples. The adjusted frequency values with the Anscombe's transformation (θ) are presented in Table 5.19. The MMD results using 15 non-metric traits for four Taiwanese Indigenous groups are presented in Table 5.20, with standard deviations presented in Table 5.21. The results show that two general clusters, Atayal-Bunun and Babuza-Pazeh, are present. It is noted that the MMD value of Atayal-Bunun and Babuza-Pazeh is smaller than twice its standard deviation, which suggests a

lack of significance in differentiating at the α=0.05 level. The dendrograms based on the MMD results are presented in Figure 5.5 (for the result of each step of the UPGMA process, see Appendix B).

The MMD results using 14 non-metric traits (removing the auditory exostosis) for four Taiwanese Indigenous groups are presented in Table 5.22, with standard deviations presented in Table 5.23. The results show that two general clusters, Atayal-Bunun and Babuza-Pazeh, are present. It is noted that the MMD value of Atayal-Bunun and Babuza-Pazeh is smaller than twice its standard deviation, which suggests a lack of significance in differentiating at the α=0.05 level. The dendrograms based on the MMD results are presented in Figure 5.6 (for the result of each step of the UPGMA process, see Appendix B).

The MMD results based on 13 traits for 8 cranial samples are presented in Table 5.24, with standard deviations presented in Table 5.25. The results show that there are two general clusters, the Taiwanese Indigenous and the Southeast Asians and the South Chinese and Okinawa groups. It is noted that the Philippines sample show a relatively similar MMD with most of the groups used in this study. The dendrogram based on the MMD results is presented in Figure 5.7 (the result of each step of the UPGMA process, see Appendix B). The Taiwanese Indigenous groups are separated from the comparative series, including the Philippines samples.

Table 5.18. Frequency of the 15 non-metric traits in 8 cranial samples.

Trait	Atayal (n=36)		Bunun (n=40)		Babuza (n=39)		Pazeh (n=33)	
	m/n	p	m/n	p	m/n	p	m/n	p
Accessory infraorbital foramen	17/36	0.472	14/40	0.350	30/39	0.769	16/33	0.485
Asterionic bone	8/36	0.222	4/40	0.100	7/39	0.179	5/33	0.152
Auditory exostosis	2/36	0.056	0/40	0	0/39	0	2/32	0.063
Biasterionic suture	10/35	0.286	7/40	0.175	1/37	0.027	1/33	0.020
Condylar canal patent	24/36	0.667	24/38	0.632	27/37	0.730	15/29	0.517
Hypoglossal canal bridging	5/36	0.139	9/40	0.225	6/37	0.162	4/32	0.125
Medial palatine canal	18/35	0.514	21/40	0.525	31/39	0.795	21/33	0.636
Metopism	2/36	0.056	2/40	0.050	1/38	0.026	4/31	0.129
Occipitomastoid bone	12/36	0.333	7/40	0.175	10/39	0.256	5/33	0.152
Ossicle at lambda	8/36	0.222	3/40	0.075	7/39	0.179	8/31	0.258
Ovale-spinosum confluence	3/36	0.083	9/40	0.225	2/39	0.051	4/33	0.121
Parietal notch bone	8/36	0.222	4/40	0.100	11/39	0.282	7/33	0.212
Supraorbital foramen	19/36	0.528	22/40	0.550	22/39	0.564	15/33	0.455
Transverse zygomatic suture	6/35	0.171	7/39	0.179	2/33	0.061	5/32	0.156
Tympanic dehiscence	0/36	0	0/40	0	4/39	0.103	7/33	0.212

*data from Fukumine *et al.* (2006)

m/n= the number of occurrences of the trait in the sample/number of the sample; p= frequency of presence

Table 5.18. (continued) Frequency of the 15 non-metric traits in 8 cranial samples.

Trait	South Chinese* (n=91)		Mainland SE Asians* (n=295)		Philippines* (n=230)		Okinawa* (n=131)	
	m/n	p	m/n	p	m/n	p	m/n	p
Accessory infraorbital foramen	-	-	-	-	-	-	-	-
Asterionic bone	31/91	0.341	78/293	0.266	63/226	0.279	21/94	0.223
Auditory exostosis	-	-	-	-	-	-	-	-
Biasterionic suture	23/91	0.253	57/293	0.159	44/228	0.193	11/101	0.109
Condylar canal patent	39/90	0.433	82/294	0.276	176/210	0.838	27/90	0.300
Hypoglossal canal bridging	11/86	0.128	46/291	0.158	46/221	0.208	16/72	0.222
Medial palatine canal	7/89	0.079	26/289	0.090	17/224	0.076	12/88	0.136
Metopism	9/91	0.099	8/295	0.027	6/230	0.026	8/122	0.066
Occipitomastoid bone	30/91	0.330	90/293	0.307	71/225	0.316	27/77	0.351
Ossicle at lambda	21/91	0.231	30/294	0.102	29/228	0.127	12/105	0.114
Ovale-spinosum confluence	6/90	0.067	18/295	0.061	14/225	0.062	3/80	0.038
Parietal notch bone	78/88	0.886	245/292	0.839	76/226	0.336	67/56	0.386
Supraorbital foramen	51/90	0.567	146/294	0.497	99/230	0.430	115/65	0.565
Transverse zygomatic suture	5/83	0.030	14/281	0.050	14/207	0.068	9/47	0.191
Tympanic dehiscence	32/90	0.356	108/294	0.367	84/226	0.372	50/100	0.500

*data from Fukumine *et al.* (2006)

m/n= the number of occurrences of the trait in the sample/number of the sample; p= frequency of presence

Table 5.19. Adjusted frequency and θ of the non-metric traits in 8 cranial samples.

Trait	Atayal		Bunun		Babuza		Pazeh	
	p	θ	p	θ	p	θ	p	θ
Accessory infraorbital foramen	0.472	0.054	0.350	0.299	0.769	-0.557	0.485	0.030
Asterionic bone	0.222	0.575	0.100	0.903	0.179	0.680	0.152	0.750
Auditory exostosis	0.056	1.057	(0.006)	1.322	(0.006)	1.319	0.063	1.025
Biasterionic suture	0.286	0.433	0.175	0.692	0.027	1.187	0.020	1.164
Condylar canal patent	0.667	-0.333	0.632	-0.261	0.730	-0.467	0.517	-0.034
Hypoglossal canal bridging	0.139	0.786	0.225	0.570	0.162	0.724	0.125	0.822
Medial palatine canal	0.514	-0.028	0.525	-0.049	0.795	-0.617	0.636	-0.270
Metopism	0.056	1.057	0.050	1.083	0.026	1.192	0.129	0.810
Occipitomastoid bone	0.333	0.333	0.175	0.692	0.256	0.498	0.152	0.750
Ossicle at lambda	0.222	0.575	0.075	0.987	0.179	0.680	0.258	0.492
Ovale-spinosum confluence	0.083	0.955	0.225	0.570	0.051	1.077	0.121	0.834
Parietal notch bone	0.222	0.575	0.100	0.903	0.282	0.442	0.212	0.598
Supraorbital foramen	0.528	-0.054	0.550	-0.098	0.564	-0.126	0.455	0.089
Transverse zygomatic suture	0.171	0.699	0.179	0.680	0.061	1.034	0.156	0.737
Tympanic dehiscence	(0.007)	1.309	(0.006)	1.322	0.103	0.894	0.212	0.598

*data from Fukumine *et al.* (2006)
p=adjusted frequency following Bartlett (1936)
θ= Anscombe's transformation

Table 5.19. (continued) Frequency and θ of the non-metric traits in 8 cranial samples.

Trait	South Chinese*		Mainland SE Asians*		Philippines*		Okinawa*	
	p	θ	p	θ	p	θ	p	θ
Accessory infraorbital foramen	-	-	-	-	-	-	-	-
Asterionic bone	0.341	0.322	0.266	0.485	0.279	0.457	0.223	0.581
Auditory exostosis	-	-	-	-	-	-	-	-
Biasterionic suture	0.253	0.513	0.159	0.655	0.193	0.659	0.109	0.889
Condylar canal patent	0.433	0.133	0.276	0.457	0.838	-0.739	0.300	0.408
Hypoglossal canal bridging	0.128	0.830	0.158	0.751	0.208	0.621	0.222	0.582
Medial palatine canal	0.079	0.989	0.090	0.958	0.076	1.007	0.136	0.805
Metopism	0.099	0.920	0.027	1.233	0.026	1.237	0.066	1.042
Occipitomastoid bone	0.330	0.345	0.307	0.395	0.316	0.376	0.351	0.300
Ossicle at lambda	0.231	0.563	0.102	0.917	0.127	0.838	0.114	0.873
Ovale-spinosum confluence	0.067	1.034	0.061	1.067	0.062	1.061	0.038	1.159
Parietal notch bone	0.886	-0.873	0.839	-0.743	0.336	0.332	0.386	-0.726
Supraorbital foramen	0.567	-0.133	0.497	0.007	0.430	0.139	0.565	-0.130
Transverse zygomatic suture	0.030	1.059	0.050	1.115	0.068	1.038	0.191	0.653
Tympanic dehiscence	0.356	0.291	0.367	0.268	0.372	0.259	0.500	0.000

*data from Fukumine *et al.* (2006)
p=adjusted frequency following Bartlett (1936)
θ= Anscombe's transformation

Table 5.20. MMD of the four Taiwan Indigenous cranial samples using 15 traits.

	Atayal	Bunun	Babuza	Pazeh
Atayal	-	0.009	0.064	0.042
Bunun		-	0.105	0.053
Babuza			-	0.030
Pazeh				-

Table 5.21. Standard deviation of the MMD of the four Taiwan Indigenous cranial samples using 15 traits.

	Atayal	Bunun	Babuza	Pazeh
Atayal	-	0.019	0.020	0.021
Bunun		-	0.019	0.021
Babuza			-	0.021
Pazeh				-

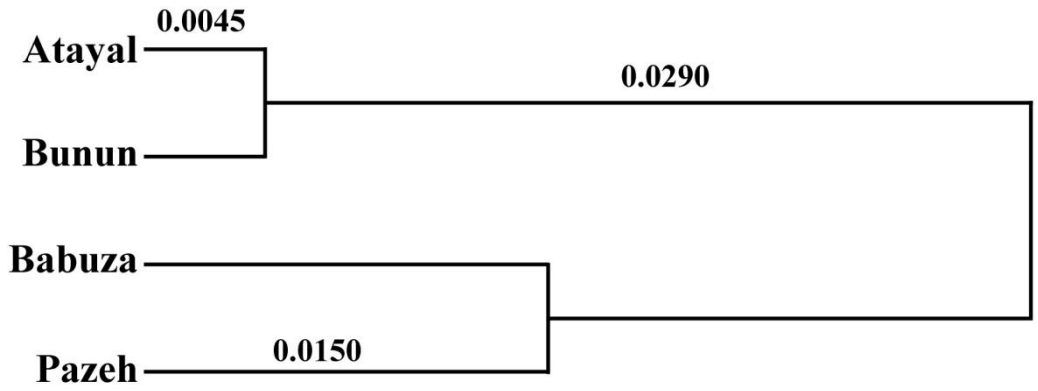

Figure 5.5. Dendrogram of the relationship of the 4 cranial samples based on MMD using 15 traits.

Table 5.22. MMD of the four Taiwan Indigenous cranial samples using 14 traits.

	Atayal	Bunun	Babuza	Pazeh
Atayal	-	0.008	0.068	0.049
Bunun		-	0.116	0.054
Babuza			-	0.030
Pazeh				-

Table 5.23. Standard deviation of the MMD of the four Taiwan Indigenous cranial samples using 14 traits.

	Atayal	Bunun	Babuza	Pazeh
Atayal	-	0.020	0.021	0.021
Bunun		-	0.019	0.021
Babuza			-	0.022
Pazeh				-

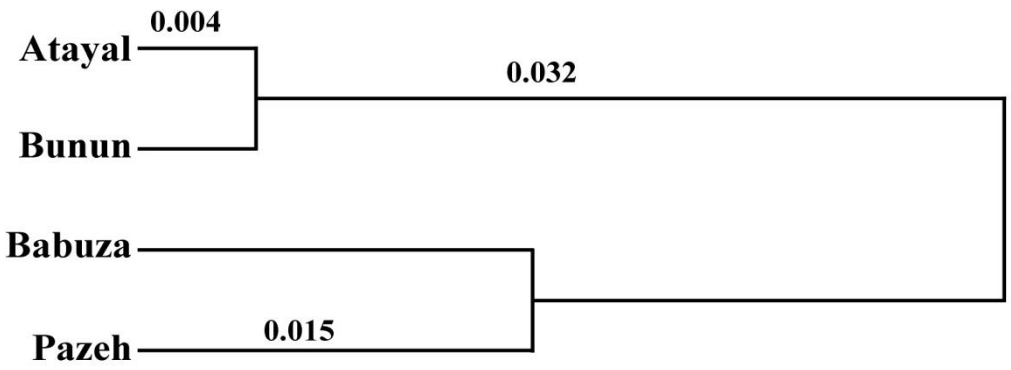

Figure 5.6. Dendrogram of the relationship of the 4 cranial samples based on MMD using 14 traits.

Table 5.24. MMD of the 8 cranial samples using 13 traits.

	Atayal	Bunun	Babuza	Pazeh	Okinawa	S. Chinese	SE. Asians	Philippines
Atayal	-	0.008	0.048	0.057	0.348	0.317	0.340	0.180
Bunun		-	0.073	0.057	0.443	0.470	0.443	0.246
Babuza			-	0.011	0.372	0.404	0.397	0.245
Pazeh				-	0.280	0.432	0.326	0.217
Okinawa					-	0.037	0.021	0.206
S. Chinese						-	0.018	0.180
SE. Asians							-	0.195
Philippines								-

Table 5.25. Standard deviation of the MMD of the 8 cranial samples using 13 traits.

	Atayal	Bunun	Babuza	Pazeh	Okinawa	S. Chinese	SE. Asians	Philippines
Atayal	-	0.021	0.021	0.023	0.016	0.015	0.012	0.013
Bunun		-	0.020	0.022	0.015	0.014	0.011	0.012
Babuza			-	0.023	0.015	0.015	0.012	0.012
Pazeh				-	0.017	0.017	0.014	0.014
Okinawa					-	0.009	0.006	0.007
S. Chinese						-	0.006	0.006
SE. Asians							-	0.003
Philippines								-

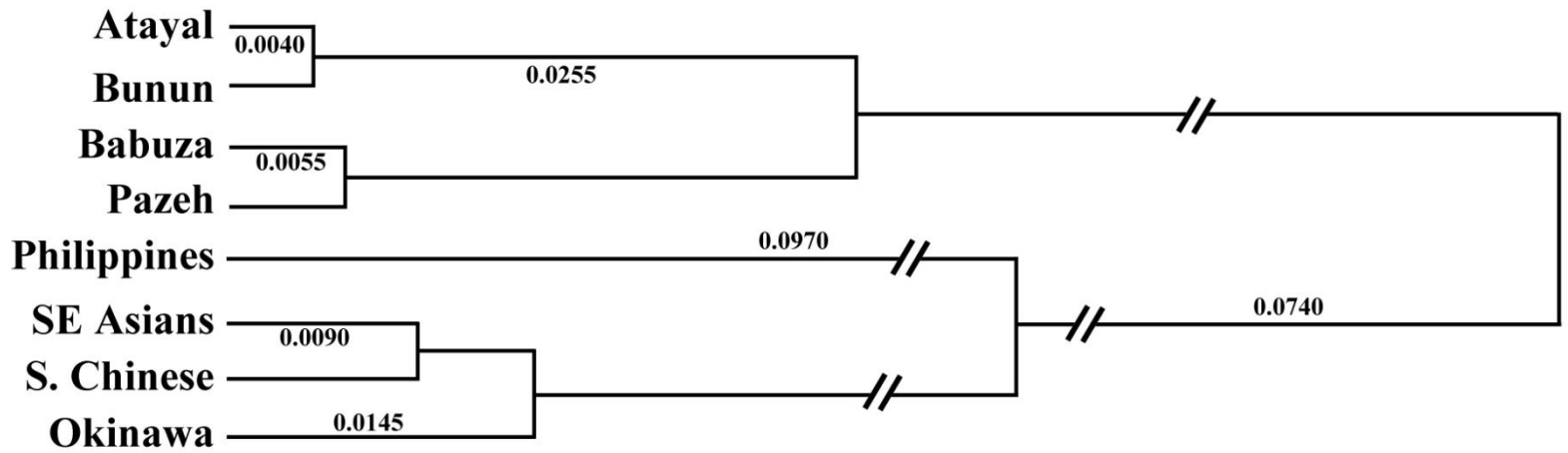

Figure 5.7. Dendrogram of the relationship of the 8 cranial samples based on MMD using 13 traits.

CHAPTER 6: DISCUSSION

Taiwanese Indigenous

As mentioned in Chapter 3, though non-metric traits tend to have lower heritability values in comparison to cranial measurements, multiple studies (e.g., Berry and Berry 1967; Cheverud and Buikstra 1981a, b, 1982; Godde 2013; Grüneberg 1963; Hanihara 2008; Hanihara *et al.* 2003; Hauser and De Stefano 1989; Leamy 1974; McGrath *et al.* 1984; Movsesian 2005; Ricaut *et al.* 2010; Richtsmeier and McGrath 1986; Stefan and Chapman 2003) had pointed out its value in studies of biodistance. The results based on craniometric and cranial non-metric traits used in this study were similar. The dendrograms based on Mahalanobis' generalized distances (Figures 5.3 and 5.4) and MMD (Figures 5.5-5.7) reveal a similar pattern of relationship. The Atayal-Bunun and Babuza-Pazeh form clusters in all dendrograms (Figures 5.3-5.7).

Stefan and Chapman (2003) utilized both craniometric and non-metric data in the samples of Marquesas Islanders and concluded that the results derived from two types of data that were similar. Rightmire (1972) also concluded that though craniometric data tend to be better, results based on craniometric and non-metric data are generally in agreement. The present study provides another example of achieving the same result regardless of the type of data.

The first discriminant function of the Taiwanese-Indigenous-group-only analysis was relatively strong in differentiating the mountain indigenous and lowland indigenous groups (Table 5.12 and Figure 5.1). The discriminant coefficients (Table 5.6) indicate that maximum cranial length (GOL), nasio-occipital length (NOL), and basion-bregma

height (BBH) are the three measurements that contribute the most to differentiating the two groups. These results confirm the general pattern of the division of the Taiwanese Indigenous groups, whereby the mountain indigenous (Atayal and Bunun) and lowland indigenous (Babuza and Pazeh) were separated geographically for a long time. Furthermore, these results also tend to support Lee's (2011) assumption that the Atayal and Bunun groups inhabited the Nantou area around 4000 B.P., while the Babuza and Pazeh groups migrated together to this area around the 19th century.

The results based on 15 and 14 non-metric traits (with and without auditory exostosis) for the four Taiwanese Indigenous samples reveal a similar result (Tables 5.20 and 5.22). This confirms the assumption discussed in Chapter 4: the influence of exposure to the cold water equally affects all four groups.

Babuza and Pazeh

Craniometric comparisons of the Taiwanese Indigenous demonstrate a close biological connection between the Babuza and Pazeh samples. The first discriminant function of the Taiwanese-Indigenous-group-only analysis was relatively strong in differentiating the Babuza and Pazeh (Table 5.12 and Figure 5.1). The discriminant coefficients (Table 5.6) indicate that maximum cranial length (GOL), nasio-occipital length (NOL), and basion-bregma height (BBH) are the three measurements that contribute the most to differentiating the two groups. As for the analysis of the seven groups, the second discriminant function was relatively strong in differentiating the Babuza and Pazeh (Table 5.13 and Figure 5.2). The discriminant coefficients (Table 5.7)

indicate that basion-bregma height (BBH), cheek height (WMH), and maximum malar length (XML) are the three measurements that contribute the most to differentiating the two groups.

However, it is noted that the Mahalanobis' generalized distance of the analysis of the seven groups are not statistically significant at the 0.01 level, which indicates the null hypothesis of "there is no significant difference between the two groups" cannot be rejected. Since the sample sizes of the two groups are relatively small, an effect of sampling fluctuations would be expected, i.e., a smaller sample size would cause the distance to differ more from zero. Therefore, the "true" biological distance may actually be closer than the result presented in Table 5.17.

This conclusion may be explained in two different ways: (1) it supports the suggestions of the collective migration during the 19th century (Hung 2006; Lee 2011), which therefore caused some admixture between the Pazeh and Babuza groups or (2) the Babuza and Pazeh groups may not differ biologically, as has been assumed. However, high percentages of the crania from the Pazeh sample were misclassified as Babuza (Table 5.14; 30.4% of Pazeh samples were classified as Babuza, while only 43.5% of the Pazeh samples were classified correctly). In contrast, the Babuza did not show this tendency (Table 5.14; 80% of the Babuza samples were classified correctly, with only three samples misclassified as Pazeh). In other words, the Pazeh samples, which were collected from the final destination of the migration event during the 19th century, show a high degree of similarity with the Babuza group, while the samples of Babuza, from the Hsilo, a habitation of the Babuza tribes before the 19th century migration, did not show

the same degree of similarity. This result contradicts the second explanation that the Babuza and Pazeh groups do not differ biologically. On the other hand, the first explanation of the collective migration may be supported based on this result, as the data may indicate that there was a transformation before and after the 19th century migration. Therefore, according to the analysis, there is some admixture between the Pazeh and Babuza at the Pazeh sample, most likely due to the 19th century migration. This conclusion also agrees with the oral history and tribal tales (Hung 2006; Lee 2011).

The results based on 15 and 14 cranial non-metric traits also indicate that the Babuza and Pazeh are closely related (Tables 5.20, 5.22, and 5.24), which is the same as the result derived from craniometric data (Tables 5.16 and 5.17). The MMD value is smaller than twice its standard deviation (Tables 5.20-5.25), which suggests that at α=0.05 level, the null hypothesis of "there is no significant difference between the two groups" cannot be rejected. This result is the same as the results based on craniometric comparisons (Table 5.17). However, as discussed above, this is most likely due to the 19th century migration.

Atayal and Bunun

Craniometric comparisons show that the Atayal and Babuza form a relatively close connection compared to other samples (Tables 5.16 and 5.17). The Atayal and Bunun cluster in the dendrogram (Figures 5.3 and 5.4) based on Mahalanobis' generalized distances. The Mahalanobis' generalized distances are statistically significant at the 0.01 level, which supports the hypothesis that the two groups were

biologically different from each other. However, the results based on cranial non-metric traits should be interpreted with caution. Although the MMD between Atayal and Bunun were close compared to other groups, the MMD value is smaller than twice its standard deviation (Tables 5.20-5.25), which indicates that at α=0.05 level, the null hypothesis of "there is no significant difference between the two groups" cannot be rejected. Again, because the sample sizes of the two groups are relatively small, an effect of sampling fluctuations is expected. Therefore, the "true" biological distance may actually be closer than the present results suggest. It is also noted, as multiple studies have pointed out (Berry and Berry 1967; Harris and Sjøvold 2004; Howe and Parsons 1967; Saunders and Rainey 2008), in biodistance studies using non-metric traits, a large number of traits should be used in order to minimize the influence of physiological and environmental factors. However, in the present study, due to the limitation of the collection, only 15 traits were used. Therefore, the results based on non-metric traits for the Atayal and Bunun samples may have two explanations: (1) the two groups were exposed to a similar environment for a long time, and therefore the effect of threshold led to the similar frequency of the traits between the two samples; or (2) since the two groups were derived from a common ancestor, traits used in the present study may not be able to differentiate the two groups. In other words, a new series of traits may need to be examined. However, the first explanation is likely to be rejected due to the complicated mountainous environment in Taiwan (see Chapter 2). Furthermore, Melton *et al.* (1998) also provides some evidence to support the second explanation. They found that the mtDNA patterns

between Atayal and Bunun (also with Ami and Paiwan, which were not analyzed in the present study) were similar, which indicates a matrilineal connection.

The second discriminant function of the Taiwanese-Indigenous-group-only analysis was relatively strong in differentiating the Atayal and Bunun (Table 5.12 and Figure 5.1). The discriminant coefficients (Table 5.6) indicate that nasio-occipital length (NOL) and maximum cranial length (GOL) are the measurements that contribute the most to differentiation. As for the analysis of the seven groups, the second discriminant function was relatively strong at differentiating the Atayal and Bunun (Table 5.13 and Figure 5.2). The discriminant coefficients (Table 5.7) indicate that basion-bregma height (BBH), cheek height (WMH), and maximum malar length (XML) are the measurements that contribute the most to differentiation. This conclusion generally agrees with the observed results by Tsai (pers. comm.), who suggests that the Atayal people tend to have a shorter cranium and flatter upper facial area when compared to the Bunun.

The general patterns of the four Taiwanese samples found in the present research are very similar to those reported in Pietrusewsky and Chang (2003). The Atayal-Bunun and Babuza-Pazeh form clusters in all dendrograms (Figures 5.3-5.7, and 6.1). The first discriminant function created in Pietrusewsky and Chang (2003) was relatively strong in differentiating the four Taiwanese Indigenous groups, with nasio-occipital length (NOL) and maximum cranial length (GOL) achieving the highest absolute coefficient values. In other words, nasio-occipital length (NOL) and maximum cranial length (GOL) are the

measurements that contribute the most to differentiation. This result shows an agreement with the present study.

In comparison to Lauer (2015), since the data of the four Taiwanese samples were also came from Chang (1993), the general patterns are also relatively similar. Lauer (2015) suggested that the Atayal samples are relatively isolated from the other Taiwanese Indigenous groups. However, the results of the present study do not show the same trend. This different result may be due to the different comparative samples used in the two studies. According to previous genetic studies (e.g., Chen *et al.* 2007; Melton *et al.* 1998), the result based on mtDNA and Y-chromosome showed some disagreement, especially in the affinity of the Atayal and Bunun. In other words, the sex difference may have caused the Atayal to be clustered differently.

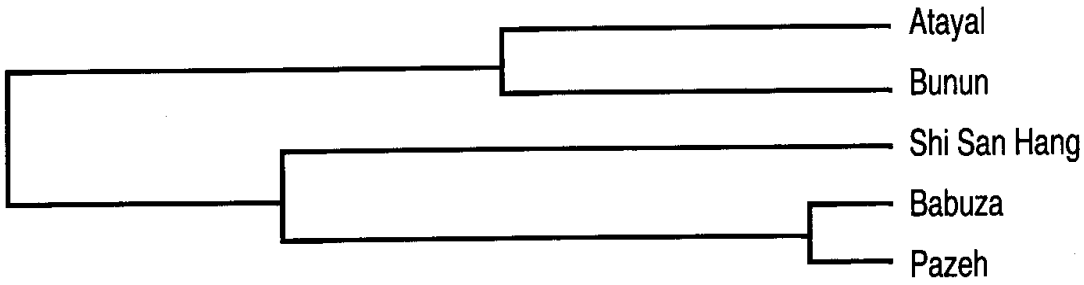

Figure 6.1. Dendrogram of the relationship of the five Taiwanese Indigenous cranial samples based on Mahalanobis' generalized distance using 29 measurements from Pietrusewsky and Chang (2003).

Regional Comparisons

The indigenous groups in Taiwan had the most diverse Austronesian languages, which suggested Taiwan as a potential homeland of the Austronesian groups (Bellwood 1988, 1991; Bellwood and Dizon 2005; Blust 1988; Diamond 2000; Dyen 1956, 1963;

Gray and Jordan 2000; Hung *et al.* 2006; Kroeber 1955; Melton *et al.* 1995, 1998; Shutler and Marck 1975; Trejaut *et al.* 2005), or at least an early stop during the dispersal of the Austronesians (Oppenheimer and Richards 2001; Solheim 1988; Su *et al.* 2000; Tsang 2012). Popular theories in regards to the diaspora of the Austronesian groups tend to assume that there was intensive migration between the Philippines and Taiwan (Figures 2.3 and 2.4). On the other hand, Pietrusewsky and Chang (2003) showed that the ultimate source of Taiwanese Indigenous population may be from eastern and northeastern Asia, while Chen (2002, 2014) and Tsang (2012) both suggested that there is little relation between Taiwan and regions to the north.

The craniometric comparisons (Table 5.17) showed that the Taiwanese Indigenous groups are relatively unrelated to the samples from South Japan. Likewise, the non-metric trait comparisons (Table 5.24) showed that the Taiwanese Indigenous groups are relatively unrelated to the samples from Okinawa. The results of the preset study support the assumption of Chen (2002, 2014) and Tsang (2012), based on archaeological evidence, that there were few connections between Taiwan and the north (South Japan and Okinawa). However, the results of the present study tend to disagree with Pietrusewsky and Chang (2003). In their analysis, the Taiwanese Indigenous groups show close connections with northeast Asian groups (including South Japan and Okinawa). Though the disagreement cannot be well explained, special attention would need to be brought to the different samples used in the two studies.

First of all, the distance from the Okinawa sample is based on non-metric traits; for the South Japan sample, 17 measurements were used in the present study, while 29

measurements were used in Pietrusewsky and Chang (2003), with only 10 measurements in common. Secondly, Pietrusewsky and Chang (2003) used more cranial series in their study. Lastly, though the collection of the Hainan and South Japan samples used in the present study were also used in the Pietrusewsky and Chang (2003) (labeled as Hainan Island and Kyushu Japanese), it is noted that only male crania were used in Pietrusewsky and Chang (2003), while a combination of both male and female were used in the present study.

As for the biological relationship between the Taiwanese Indigenous groups and the Philippines, the results from the craniometric data (Table 5.17; Figures 5.2 and 5.4) and non-metric data (Table 5.24; Figure 5.7) show a similar pattern. The Philippines groups showed a distant relationship with the Taiwanese Indigenous groups and were placed in a different cluster from the Taiwanese Indigenous groups. In other words, the results did not show a close affinity as expected in the hypothesis where Taiwan is the origin of people from the Philippines or the Philippines is the origin of the groups from Taiwan. The hypothesis indicates a closer biological affinity between Taiwanese Indigenous groups and the Philippines. If groups migrated between the two areas, the intensive gene flow would cause them to be clustered together. However, Figures 5.2, 5.4, and 5.7 showed a different pattern than expected, which tends to not agree with the hypothesis. In fact, these results tend to support the assumption by Tsang (2012), who generated data from different sources (e.g., archaeological records) and suggested that populations from Taiwan and the Philippines may share a common ancestor who

migrated by different routes to Taiwan and the Philippines separately. Therefore, they clustered separately.

Although the results may support the assumption of multiple migration routes, the influences of the migration of the Chinese people cannot be ignored. People from mainland China (especially the southeast coast) had a long history of migration, especially after 1567, when the prohibition on emigration was removed (Zhuang 2008). Since then, a large amount of Chinese (mostly Han Chinese) moved to Southeast Asia, including the Philippines, and the specimens from the Philippines may be admixture with the Chinese people. It is noted that the Howells' data came from dead prisoners from Manila before the Second World War, while Fukumine *et al.* (2006) used native people from the Philippines. Nevertheless, the effect of Chinese immigration should be considered. On the other hand, though Turner and Lien (1984) pointed out that while the Taiwanese Indigenous people may also have been influenced by the mainland Chinese, this influence may be relatively ancient (4000 BP) and perhaps limited.

Based on craniometric results (Table 5.17), the Philippines is closest to the Hainan. Similarly, the results derived from non-metric traits (Table 5.24) indicate that the groups from the Philippines also had a close relationship with the South Chinese. The close biological affinity may be explained as a continuity of a common ancestor or it may be a result of later admixture. Therefore, the influence of Chinese immigration should be carefully considered.

Although clustered with the Chinese-related groups (South Chinese, Southeast Asians and Okinawa), the relationship between the Philippines and the Chinese-related

group cluster is distant (Figure 5.7). This suggests that though the sample may be affected by Chinese immigration, the influence is limited in the Fukumine *et al.* (2006) sample, which fits with the provenience information. Therefore, based on the results presented in Figure 5.7, which utilized the Fukumine *et al.* (2006) samples, a clear separation between the Philippines and the Taiwanese Indigenous groups is shown. In other words, this finding tends to fit with the pattern that generated from Tsang's (2012) assumption of multiple routes of dispersal.

In regards to the possible homeland of the Taiwanese Indigenous groups, recent archaeological evidence shows that there are some similarities between the Neolithic sites in Taiwan (Tapenkeng Culture) and sites around the Canton River (Tsang *et al.* 2006). Lauer (2015) also pointed out that the Neolithic Taiwanese Indigenous groups may share a common Southeast China regional origin with samples from Dingsishan, a Southeast China riverine Neolithic group. Therefore, a potential source of the Taiwanese Indigenous groups may be the southern coastal area of mainland China, around the Canton River. However, this hypothesis cannot be examined in the present study due to the lack of appropriate samples from the Canton River. Future research utilizing more samples from the southern coastal area of mainland China would be beneficial to the investigation of the origin of Taiwanese Indigenous groups.

CHAPTER 7: CONCLUSIONS

The purpose of the present study was to measure the degree of biological affinity between the Taiwanese Indigenous groups. Previous studies based on linguistics, ethnography, and archaeology showed that there are differences between the indigenous groups in Taiwan. In the present study, craniometric and non-metric cranial trait data recorded in four Taiwanese Indigenous groups (Atayal, Bunun, Babuza, and Pazeh) from modern collections were analyzed in order to examine the biological relationship of some Taiwanese Indigenous groups. Two hypotheses were proposed. First, the Taiwanese Indigenous groups would have significant biological differences and that there would be a distinct difference between the mountain indigenous (Atayal and Bunun) and the lowland indigenous (Babuza and Pazeh) groups. Second, limited comparisons with groups from other areas were made in order to examine the possible dispersal pattern of the Taiwanese Indigenous groups. It was hypothesized that the Taiwanese Indigenous groups would show the closest affinity with the samples from the Philippines, while the other groups would be in another cluster based on the major hypothesis of the Austronesians' origin.

The first hypothesis that the Taiwanese Indigenous groups are not just a linguistic or cultural group but actually differ biologically is supported in the present study, especially by the craniometric data. Based on the results, there is a statistically significant difference between the Taiwanese Indigenous groups. In other words, the traditional division of Taiwanese Indigenous groups also had a biological basis. Furthermore, the biological connections and differentiation of the mountain (Atayal and

Bunun) and lowland (Babuza and Pazeh) groups, found in this research, are in agreement with linguistic, ethnographic, and mtDNA evidence.

Basion-bregma height (BBH), bimaxillary breadth (ZMB), and bijugal breadth (JUB) are the three most important measurements differentiating the four Taiwanese Indigenous groups used in this study. Three measurements that contribute the most to differentiating mountain indigenous groups and lowland indigenous groups are: maximum cranial length (GOL), nasio-occipital length (NOL), and basion-bregma height (BBH). Maximum cranial length (GOL), nasio-occipital length (NOL), and basion-bregma height (BBH) are the measurements with the highest contribution in differentiating the Babuza and Pazeh groups. The nasio-occipital length (NOL) and maximum cranial length (GOL) are the measurements that contribute the most in differentiating Atayal and Bunun groups.

The cross-validation results of the craniometric analysis also support linguistic and oral historical evidence that suggests that the Babuza and Pazeh groups together migrated to central Taiwan around the 19th century. The results also indicate that some unknown environmental factors and/or sex differences may explain the minor differences between the results of metric and non-metric data analyses. This may be examined using Atayal and Bunun samples from different areas in future studies.

It is noted that the results based on craniometric and cranial non-metric traits in the analysis of the four Taiwanese Indigenous groups showed similar patterns of relatedness. The Atayal and Bunun are biologically close, while the Babuza and Pazeh

form a second grouping. This result provides another example of achieving the same result regardless of the type of data.

The results of the present study do not support a close relationship between Taiwanese Indigenous groups and the groups from the Philippines. These findings do not support theories that favor intensive migration between the Philippines and Taiwan during the diaspora of Austronesian-speaking groups. The present research may support archaeological evidence that the early dispersal of Austronesian groups may have occurred several times through multiple routes to Taiwan and the Philippines. The results of the present study also indicate that the Taiwanese Indigenous groups had little connection with groups to the north of Taiwan, including the Yangtze River region (south Chinese sample). Due to the limitations of the sample size and number of comparative groups used in the present study, the results of external connections must be viewed with caution.

Future Research

Future research based on the present study should be cautious when using recent inhabitants as samples due to the previously discussed complications (see Chapters 1, 2, and 4); for example, increased mixing and the influence of government. Based on the findings of the present study, it is recommended that prehistoric archaeological remains be used. Previous cemeteries may also be a useful source for Taiwanese Indigenous samples. However, most of them are poorly preserved, which makes craniometric analyses extremely difficult. The present study showed that the conclusions driven from craniometric data and non-metric data are generally in agreement, which provides some

validation for using non-metric data in investigating biological affinity of the Taiwanese Indigenous groups. The successful use of non-metric data in addressing the questions of population history and structure of the Taiwanese Indigenous may thus help in expanding the number of samples to be analyzed. However, based on the result of Atayal and Bunun, it may be necessary to use additional and/or different non-metric traits. It is also noted that due to the limitation of the sample size and the completeness of each individual, male and female data were combined in the present study. However, based on the disagreement in results from genetic research (e.g., Chen *et al.* 2007; Melton *et al.* 1995, 1998; Mirabal *et al.* 2013; Su *et al.* 2000 Trejaut *et al.* 2005), it is recommended that sex-specific analyses be made when more data are available. While the present study made comparisons with samples from neighboring regions, it is noted that a small number of cranial series were used in the present study. Therefore, the utilization of more samples in future studies is recommended in order to establish more concrete findings.

APPENDIX A: CLUSTER ANALYSIS (CRANIOMETRIC DATA)

Table A.1. Mahalanobis' generalized distance using 9 c-scores representing 9 measurements in the analysis of the four Taiwanese Indigenous groups.

Groups	Atayal	Bunun	Babuza	Pazeh
Atayal	-	5.915	11.625	7.264
Bunun		-	10.684	8.530
Babuza				4.041*
Pazeh				-

* the smallest value

Table A.2. First clustering of the UPGMA process.

Groups	Atayal	Bunun	(Babuza, Pazeh)
Atayal	-	5.915*	9.458
Bunun		-	9.601
(Babuza, Pazeh)			-

* the smallest value

Table A.3. Second clustering of the UPGMA process.

Groups	(Atayal, Bunun)	(Babuza, Pazeh)
(Atayal, Bunun)	-	9.532
(Babuza, Pazeh)		-

* the smallest value

Table A.4. Mahalanobis' generalized distance using 17 c-scores representing 17 measurements in the analysis of seven groups.

Groups	Atayal	Bunun	Babuza	Pazeh	S. Japan	Hainan	Philippines
Atayal	-	5.457	12.685	8.906	23.401	23.879	27.325
Bunun		-	20.548	18.903	32.110	31.843	35.636
Babuza			-	4.435	23.544	16.173	36.261
Pazeh				-	16.853	10.298	17.994
S. Japan					-	3.489*	4.271
Hainan						-	3.857
Philippines							-

* the smallest value

Table A.5. First clustering of the UPGMA process.

Groups	Atayal	Bunun	Babuza	Pazeh	(S. Japan, Hainan)	Philippines
Atayal	-	5.457	12.685	8.906	23.640	27.325
Bunun		-	20.548	18.903	31.977	35.636
Babuza			-	4.435	19.858	36.261
Pazeh				-	13.575	17.994
(S. Japan, Hainan)					-	4.064*
Philippines						-

* the smallest value

Table A.6. Second clustering of the UPGMA process.

Groups	Atayal	Bunun	Babuza	Pazeh	[(S. Japan, Hainan), Philippines]
Atayal	-	5.457	12.685	8.906	24.868
Bunun		-	20.548	18.903	33.196
Babuza			-	4.435*	25.326
Pazeh				-	15.048
[(S. Japan, Hainan), Philippines]					-

* the smallest value

Table A.7. Third clustering of the UPGMA process.

Groups	Atayal	Bunun	(Babuza, Pazeh)	[(S. Japan, Hainan), Philippines]
Atayal	-	5.457*	10.796	24.868
Bunun		-	19.726	33.196
(Babuza, Pazeh)			-	20.187
[(S. Japan, Hainan), Philippines]				-

* the smallest value

Table A.8. Fourth clustering of the UPGMA process.

Groups	(Atayal, Bunun)	(Babuza, Pazeh)	[(S. Japan, Hainan), Philippines]
(Atayal, Bunun)	-	15.261*	29.032
(Babuza, Pazeh)		-	20.187
[(S. Japan, Hainan), Philippines]			-

* the smallest value

Table A.9. Fifth clustering of the UPGMA process.

Groups	[(Atayal, Bunun), (Babuza, Pazeh)]	[(S. Japan, Hainan), Philippines]
[(Atayal, Bunun), (Babuza, Pazeh)]	-	24.610
[(S. Japan, Hainan), Philippines]		-

* the smallest value

APPENDIX B: CLUSTER ANALYSIS (NON-METRIC DATA)

Table B.1. Mean Measure of Divergence for the four Taiwanese Indigenous cranial samples using 15 traits.

	Atayal	Bunun	Babuza	Pazeh
Atayal	-	0.009*	0.064	0.042
Bunun		-	0.105	0.053
Babuza			-	0.030
Pazeh				-

* the smallest value

Table B.2. First clustering of the UPGMA process.

	(Atayal, Bunun)	Babuza	Pazeh
(Atayal, Bunun)	-	0.085	0.048
Babuza		-	0.030*
Pazeh			-

* the smallest value

Table B.3. Second clustering of the UPGMA process.

	(Atayal, Bunun)	(Babuza, Pazeh)
(Atayal, Bunun)	-	0.067
(Babuza, Pazeh)		-

* the smallest value

Table B.4. Mean Measure of Divergence for the four Taiwanese Indigenous cranial samples using 14 traits.

	Atayal	Bunun	Babuza	Pazeh
Atayal	-	0.008*	0.068	0.049
Bunun		-	0.116	0.054
Babuza			-	0.030
Pazeh				-

* the smallest value

Table B.5. First clustering of the UPGMA process.

	(Atayal, Bunun)	Babuza	Pazeh
(Atayal, Bunun)	-	0.092	0.052
Babuza		-	0.030*
Pazeh			-

* the smallest value

Table B.6. Second clustering of the UPGMA process.

	(Atayal, Bunun)	(Babuza, Pazeh)
(Atayal, Bunun)	-	0.072
(Babuza, Pazeh)		-

* the smallest value

Table B.7. Mean Measure of Divergence for the 8 cranial samples using 13 traits.

	Atayal	Bunun	Babuza	Pazeh	Okinawa	S. Chinese	SE. Asians	Philippines
Atayal	-	0.008*	0.048	0.057	0.348	0.317	0.340	0.180
Bunun		-	0.073	0.057	0.443	0.470	0.443	0.246
Babuza			-	0.011	0.372	0.404	0.397	0.245
Pazeh				-	0.280	0.432	0.326	0.217
Okinawa					-	0.037	0.021	0.206
S. Chinese						-	0.018	0.180
SE. Asians							-	0.195
Philippines								-

* the smallest value

Table B.8. First clustering of the UPGMA process.

	(Atayal, Bunun)	Babuza	Pazeh	Okinawa	S. Chinese	SE. Asians	Philippines
(Atayal, Bunun)	-	0.061	0.057	0.396	0.394	0.392	0.213
Babuza		-	0.011*	0.372	0.404	0.397	0.245
Pazeh			-	0.280	0.432	0.326	0.217
Okinawa				-	0.037	0.021	0.206
S. Chinese					-	0.018	0.180
SE. Asians						-	0.195
Philippines							-

* the smallest value

Table B.9. Second clustering of the UPGMA process.

	(Atayal, Bunun)	(Babuza, Pazeh)	Okinawa	S. Chinese	SE. Asians	Philippines
(Atayal, Bunun)	-	0.059	0.396	0.394	0.392	0.213
(Babuza, Pazeh)		-	0.326	0.418	0.362	0.231
Okinawa			-	0.037	0.021	0.206
S. Chinese				-	0.018*	0.180
SE. Asians					-	0.195
Philippines						-

* the smallest value

Table B.10. Third clustering of the UPGMA process.

	(Atayal, Bunun)	(Babuza, Pazeh)	Okinawa	(S. Chinese, SE. Asians)	Philippines
(Atayal, Bunun)	-	0.059	0.396	0.393	0.213
(Babuza, Pazeh)		-	0.326	0.390	0.231
Okinawa			-	0.029*	0.206
(S. Chinese, SE. Asians)				-	0.188
Philippines					-

* the smallest value

Table B.11. Fourth clustering of the UPGMA process.

	(Atayal, Bunun)	(Babuza, Pazeh)	[Okinawa, (S. Chinese, SE. Asians)]	Philippines
(Atayal, Bunun)	-	0.059*	0.394	0.213
(Babuza, Pazeh)		-	0.369	0.231
[Okinawa, (S. Chinese, SE. Asians)]			-	0.194
Philippines				-

* the smallest value

Table B.12. Fifth clustering of the UPGMA process.

	[(Atayal, Bunun), (Babuza, Pazeh)]	[Okinawa, (S. Chinese, SE. Asians)]	Philippines
[(Atayal, Bunun), (Babuza, Pazeh)]	-	0.382	0.222
[Okinawa, (S. Chinese, SE. Asians)]		-	0.194*
Philippines			-

* the smallest value

Table B.13. Sixth clustering of the UPGMA process.

	[(Atayal, Bunun), (Babuza, Pazeh)]	{[Okinawa, (S. Chinese, SE. Asians)], Philippines}
[(Atayal, Bunun), (Babuza, Pazeh)]	-	0.342
{Philippines, [Okinawa, (S. Chinese, SE. Asians)]}		-

* the smallest value

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